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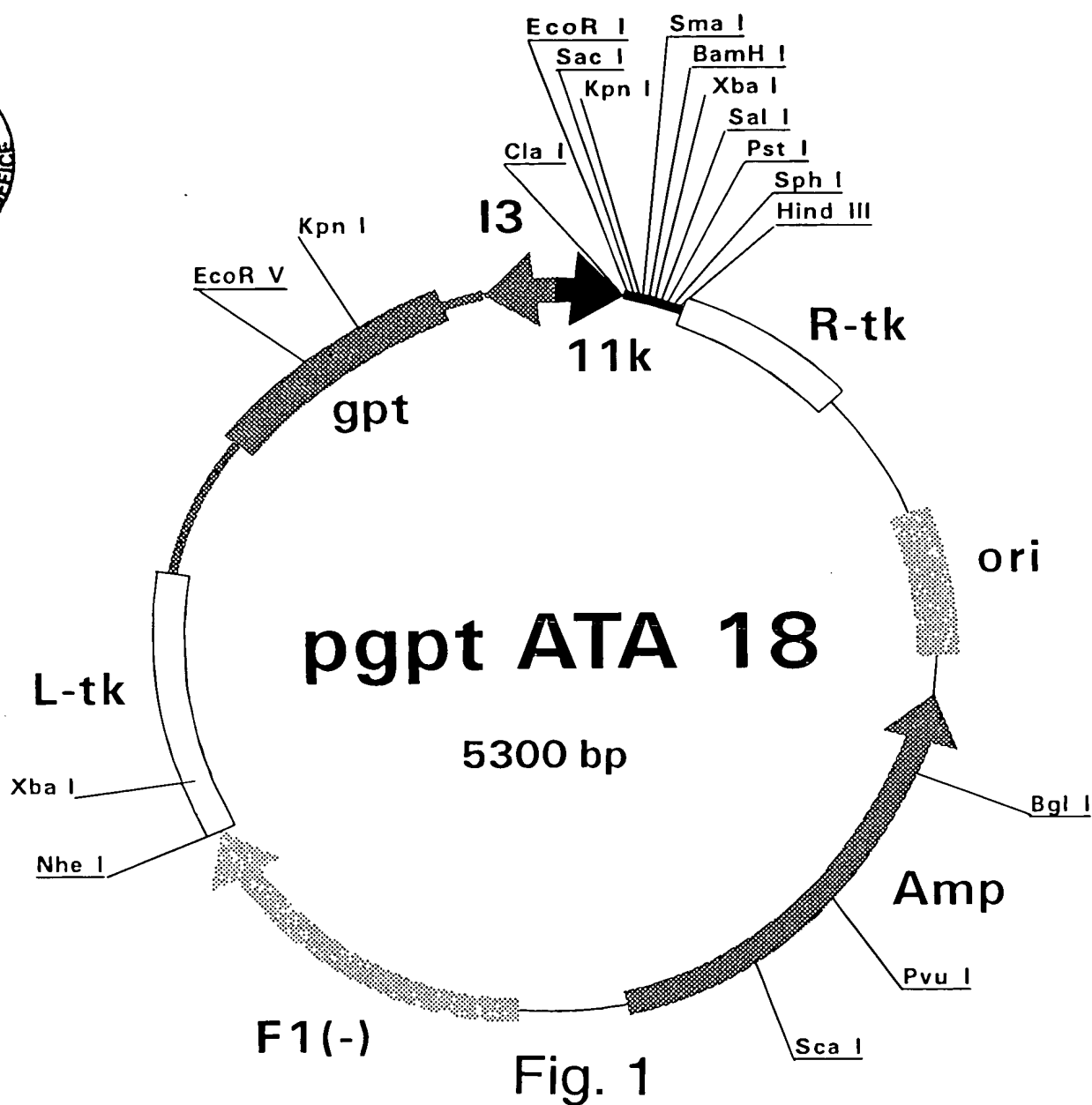
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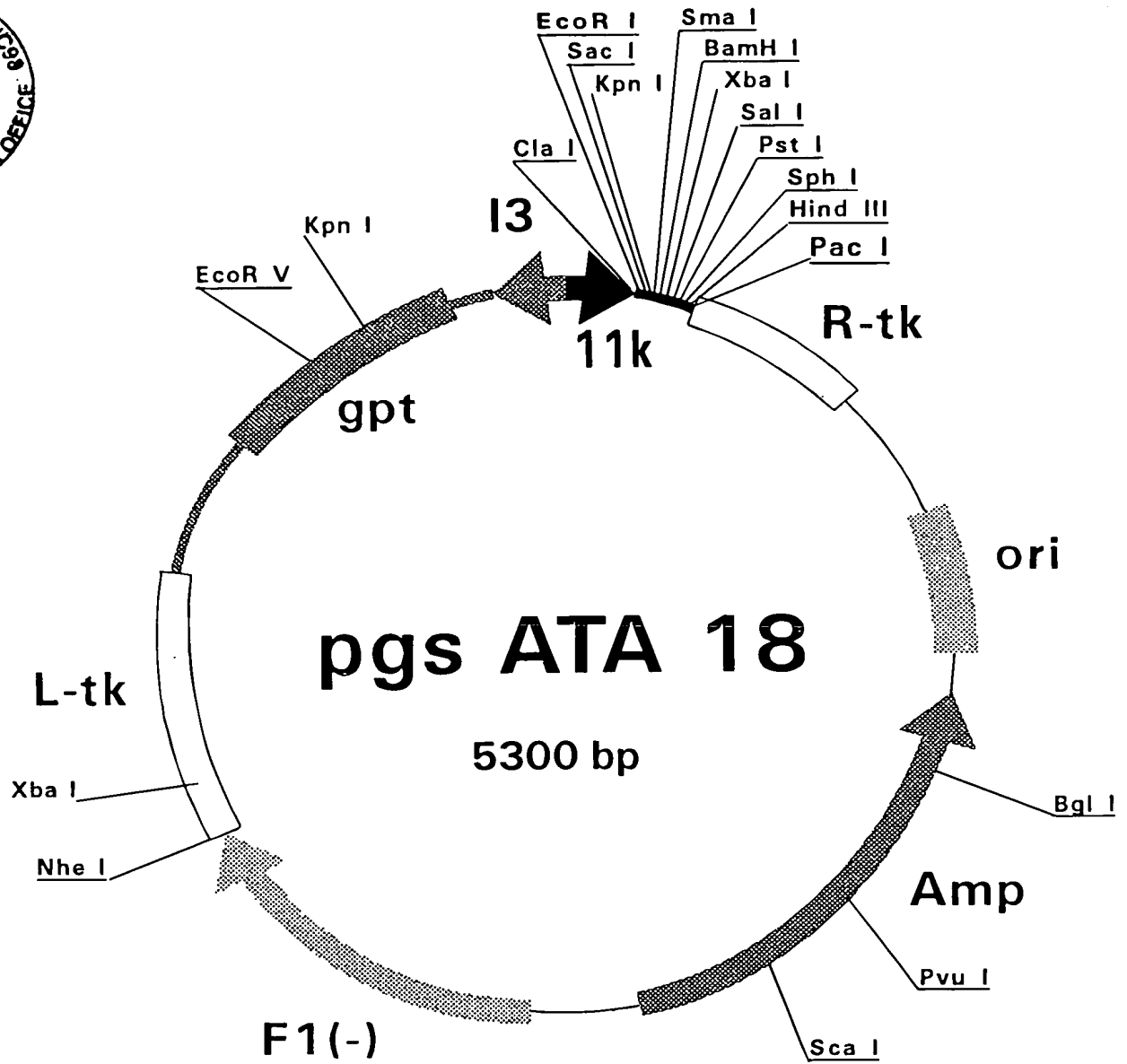


Fig. 2

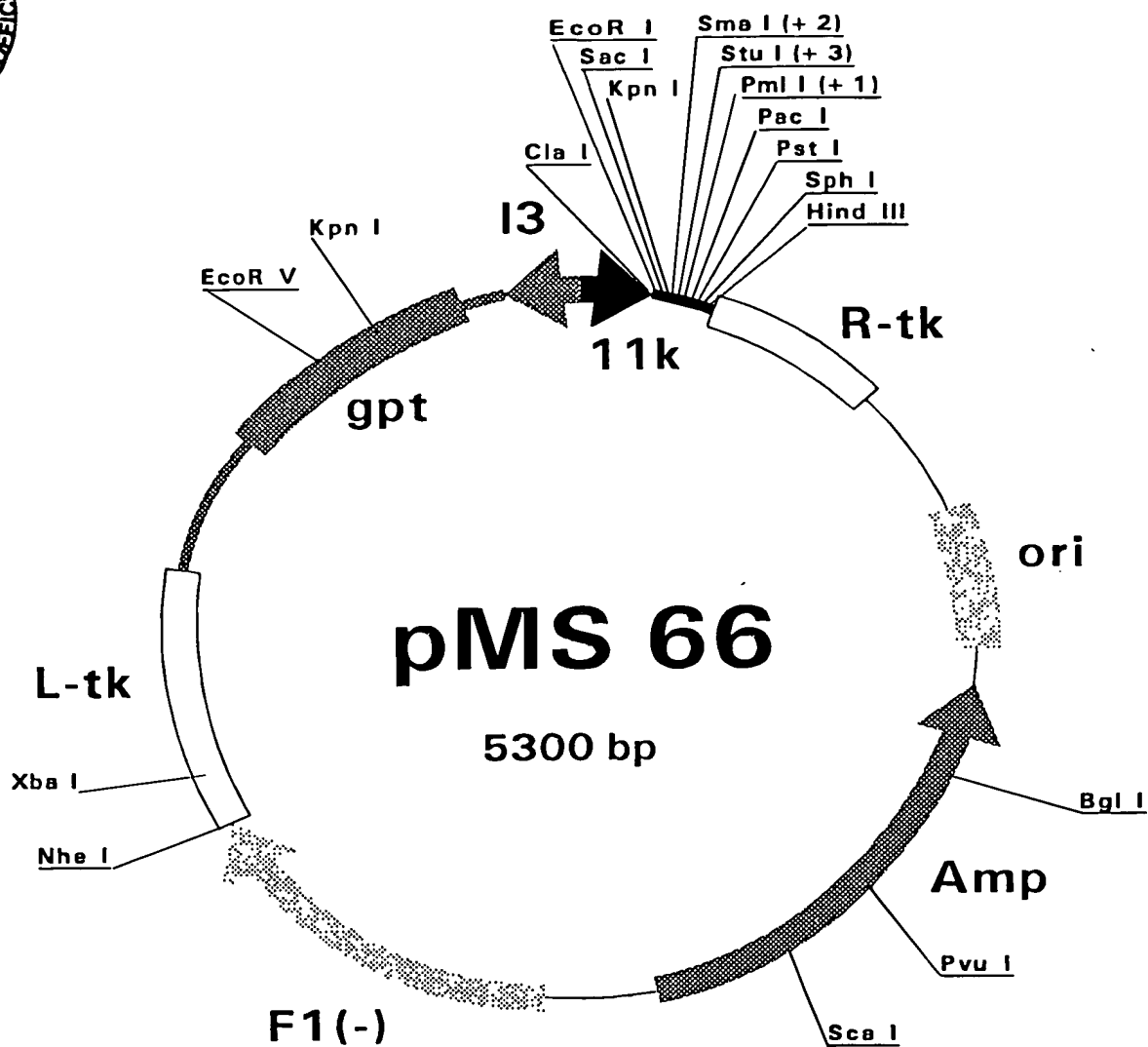


Fig. 3

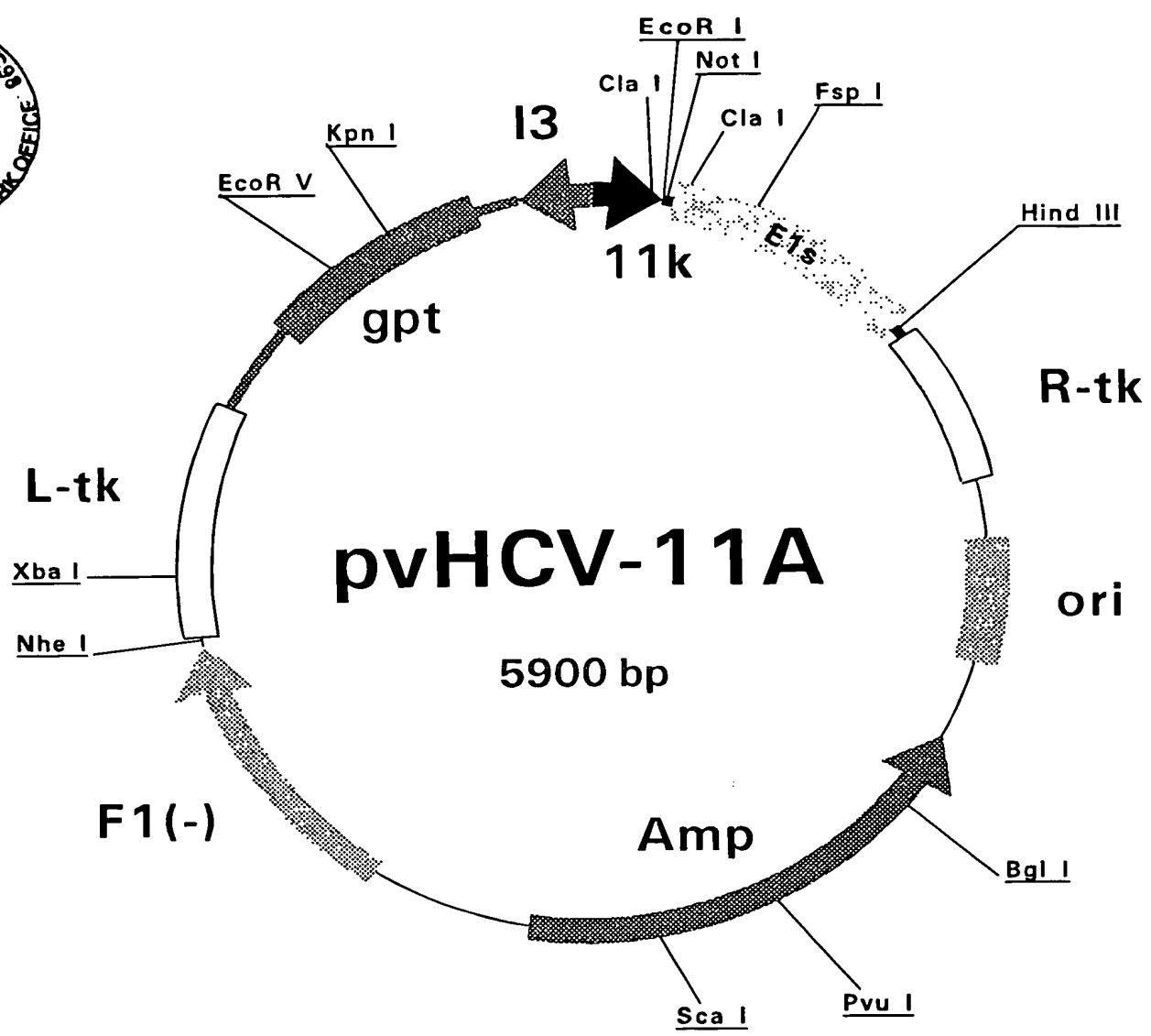
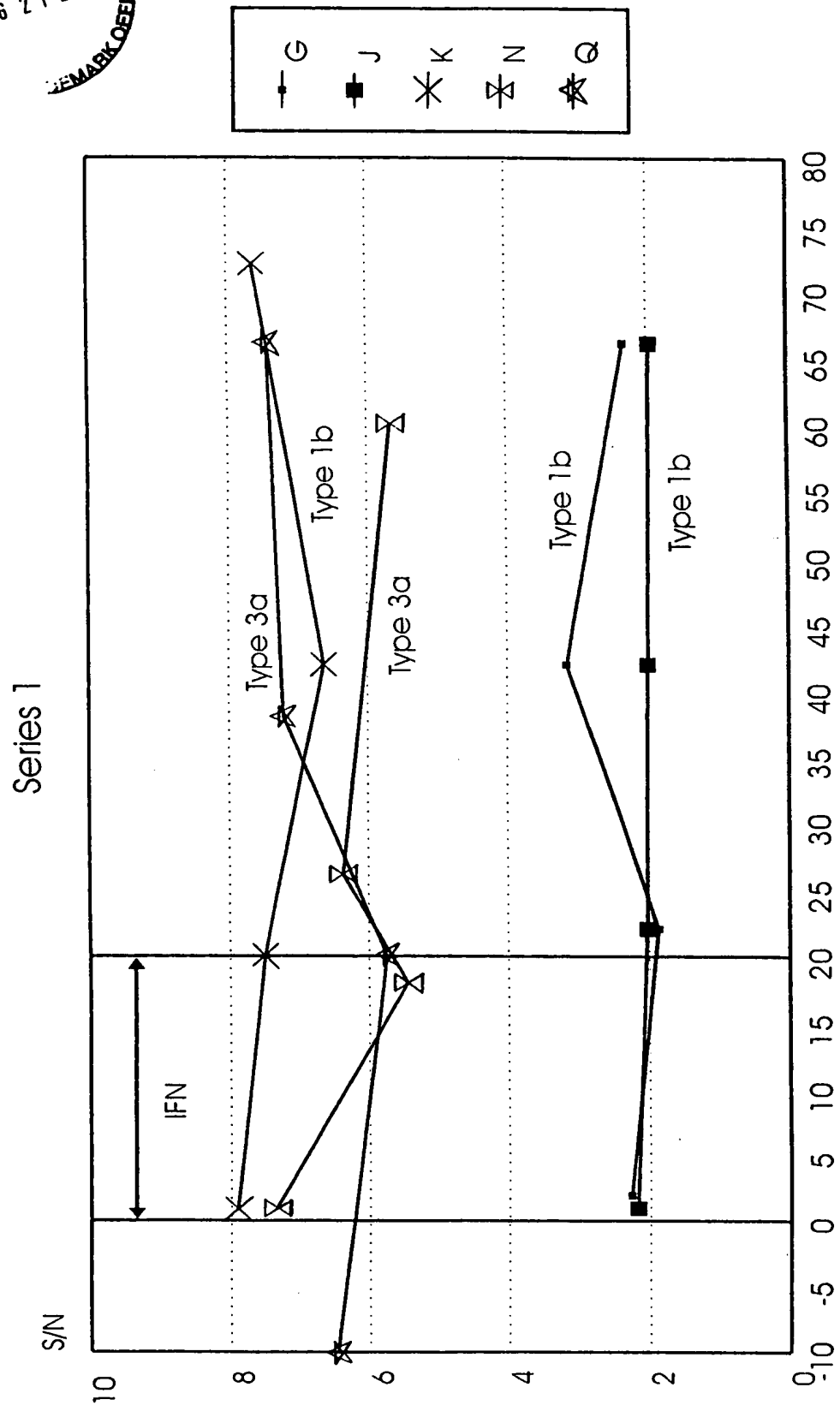


Fig. 4

Anti-E1 levels in NON-responders to IFN treatment



weeks after start of treatment

Fig. 5



Anti-E1 levels in RESPONDERS to IFN treatment

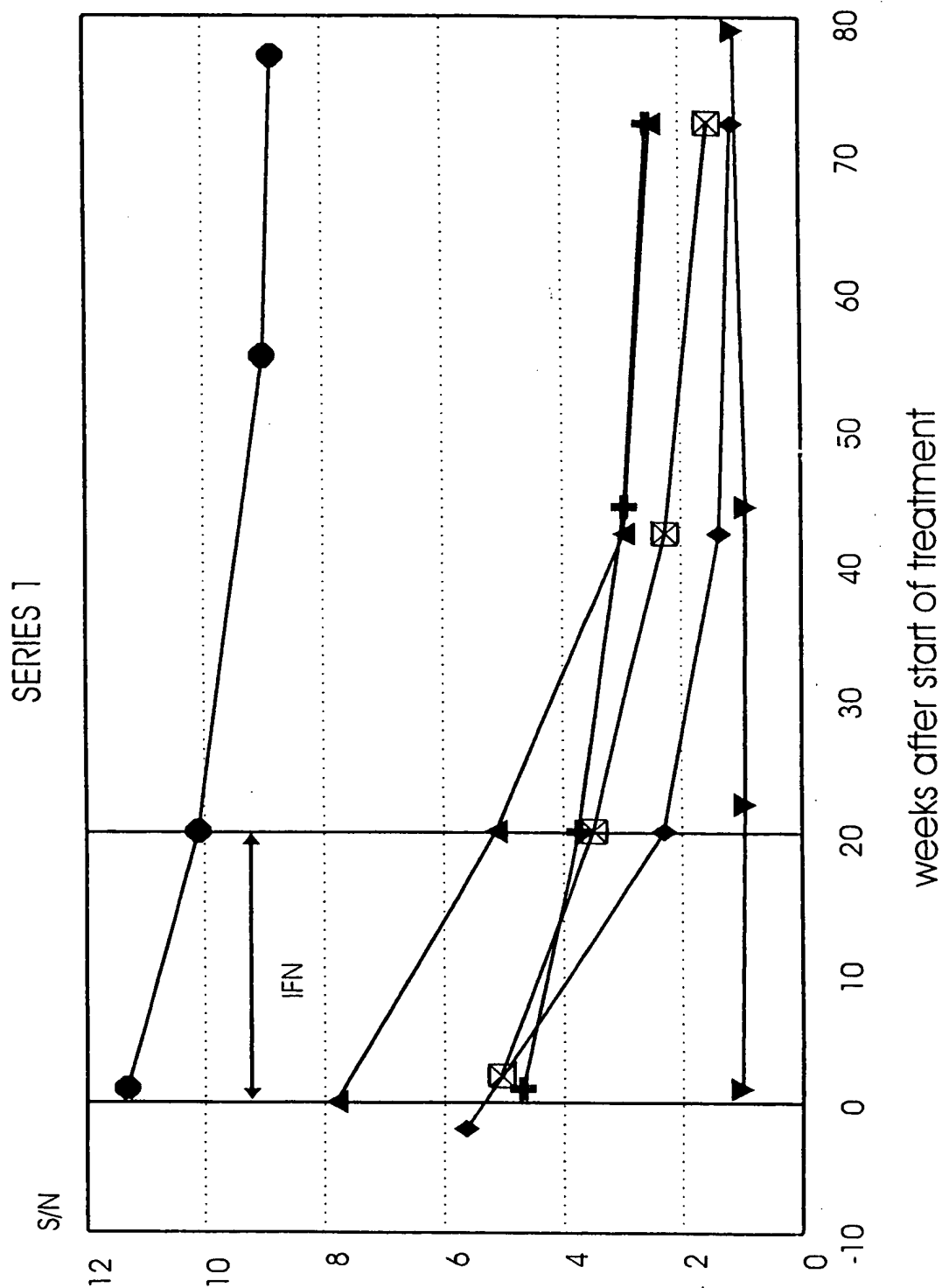
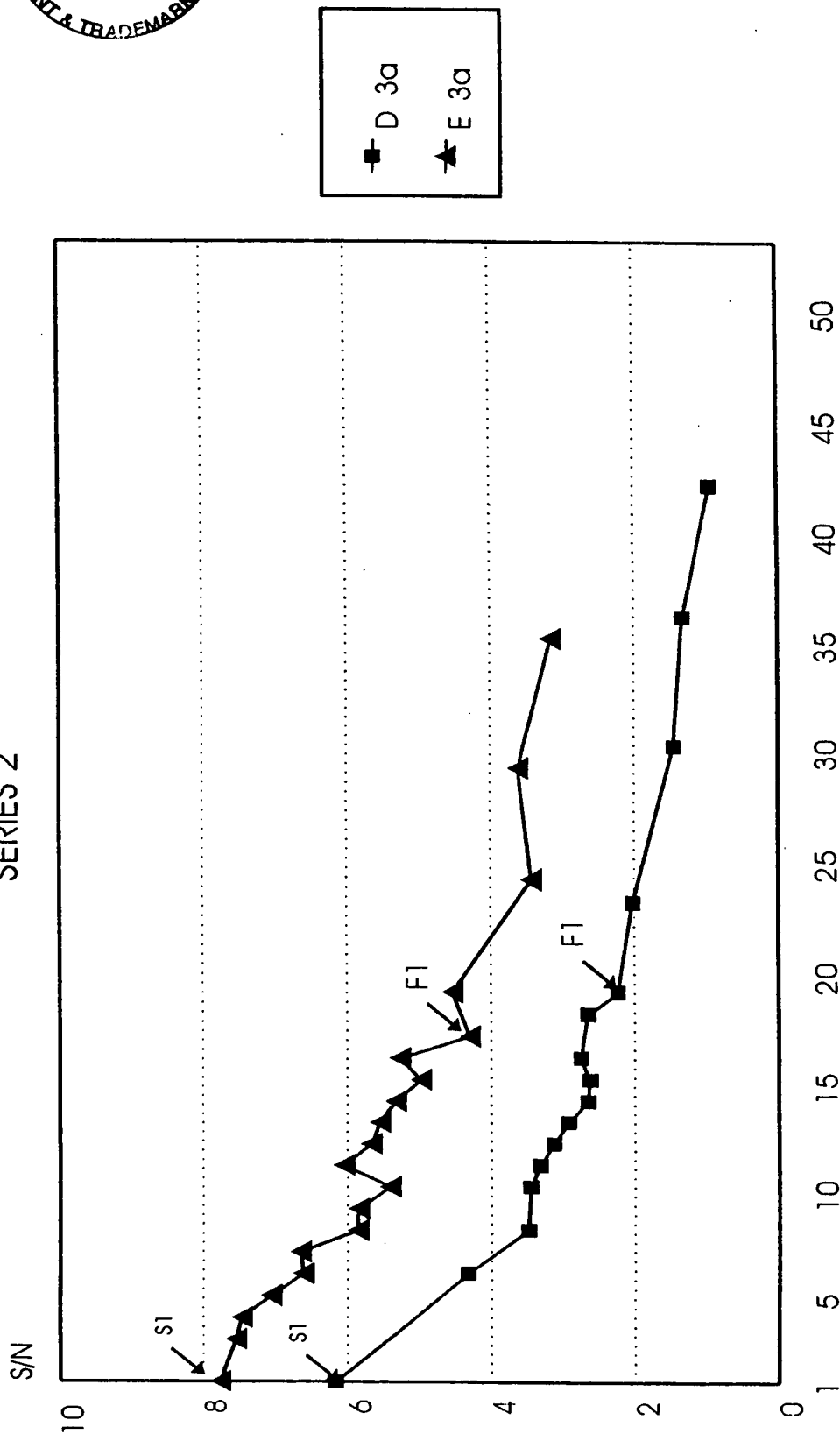


Fig. 6

Anti-E1 levels in patients with COMPLETE response to IFN

SERIES 2



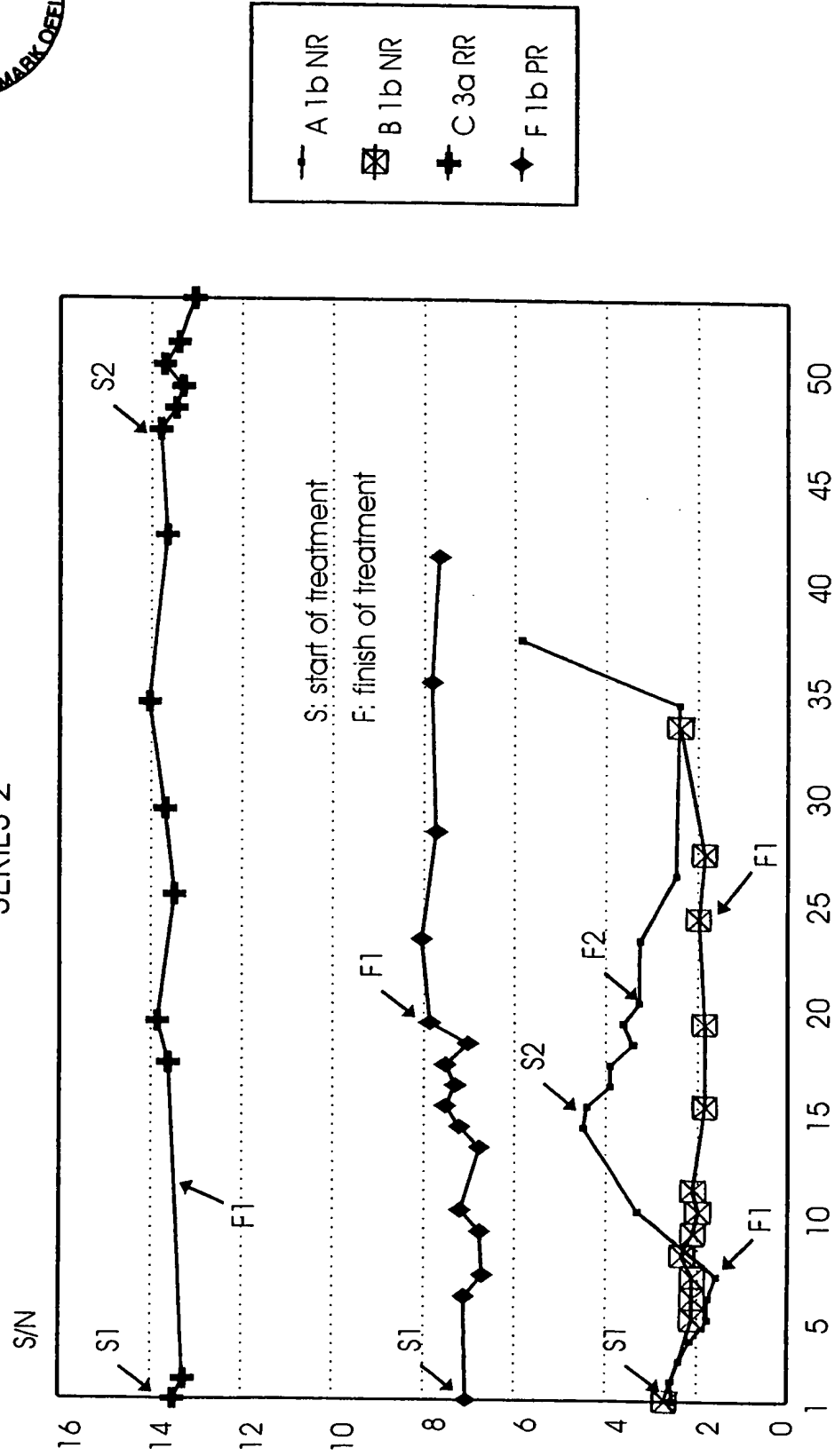
months after start of treatment

Fig. 7



Anti-E1 levels in INCOMPLETE responders to IFN treatment

SERIES 2

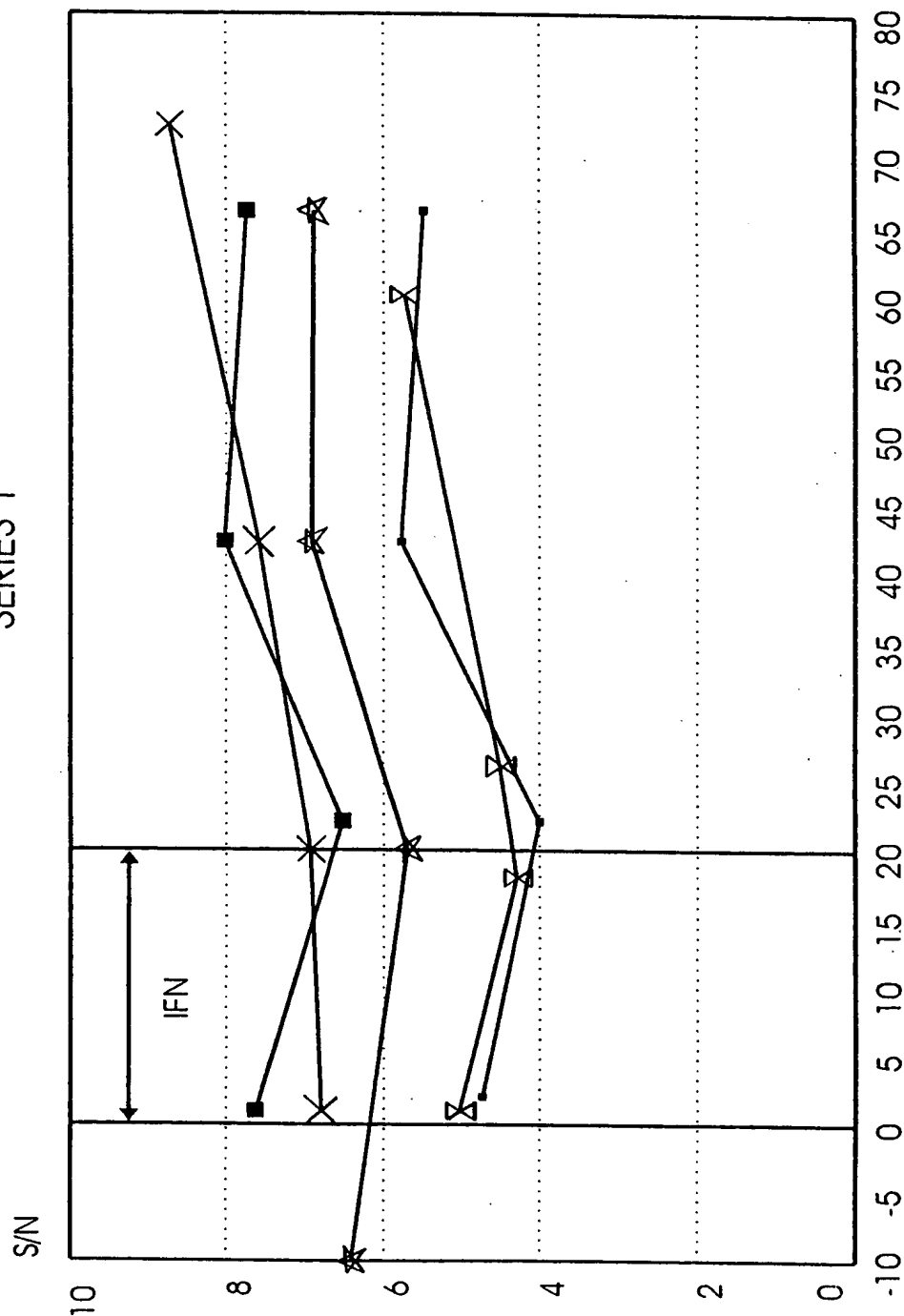


months after start of treatment

Fig. 8

Anti-E2 levels in NON-RESPONDERS to IFN treatment

SERIES 1

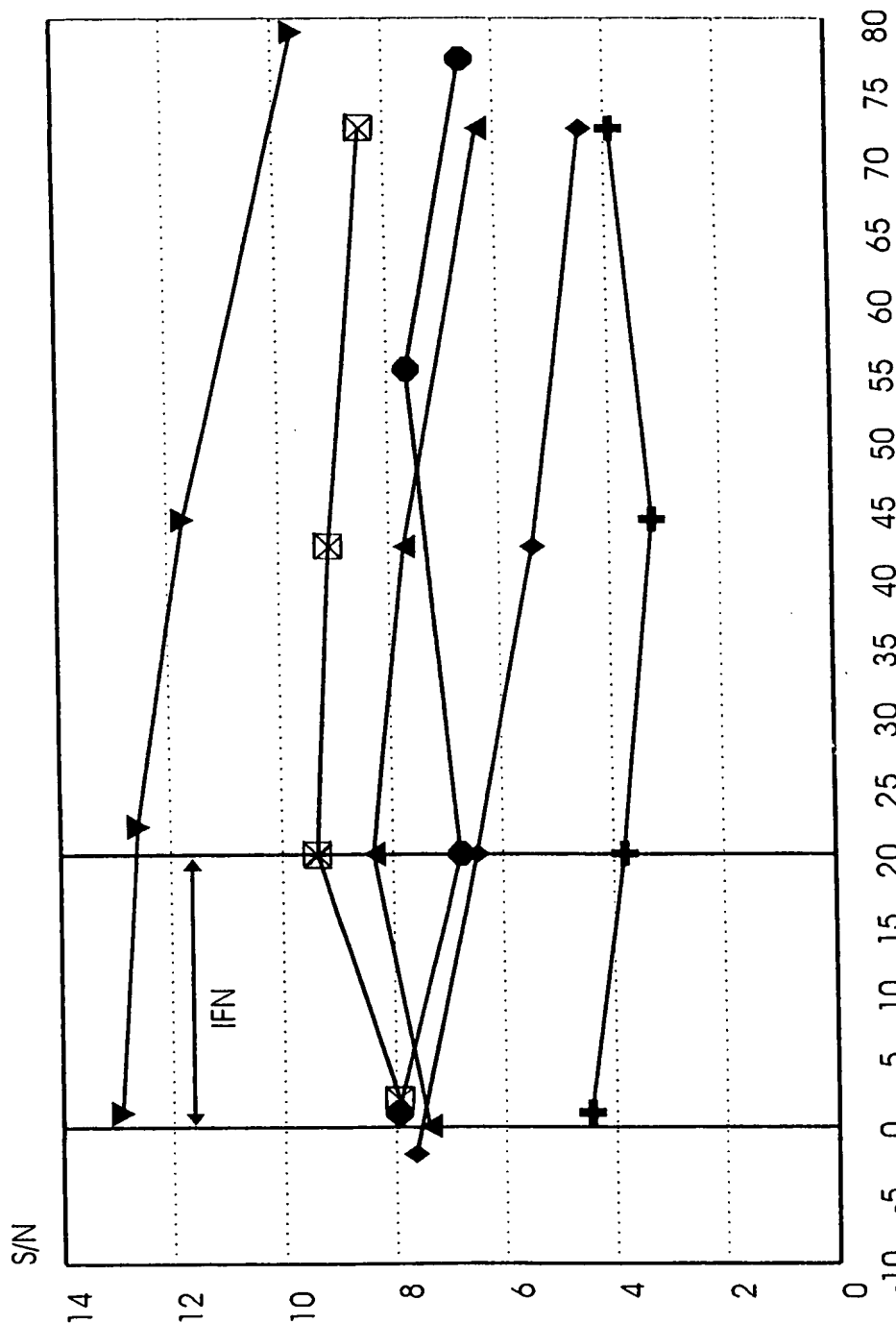


weeks after start of treatment

Fig. 9

Anti-E2 levels in RESPONDERS to IFN treatment

SERIES 1

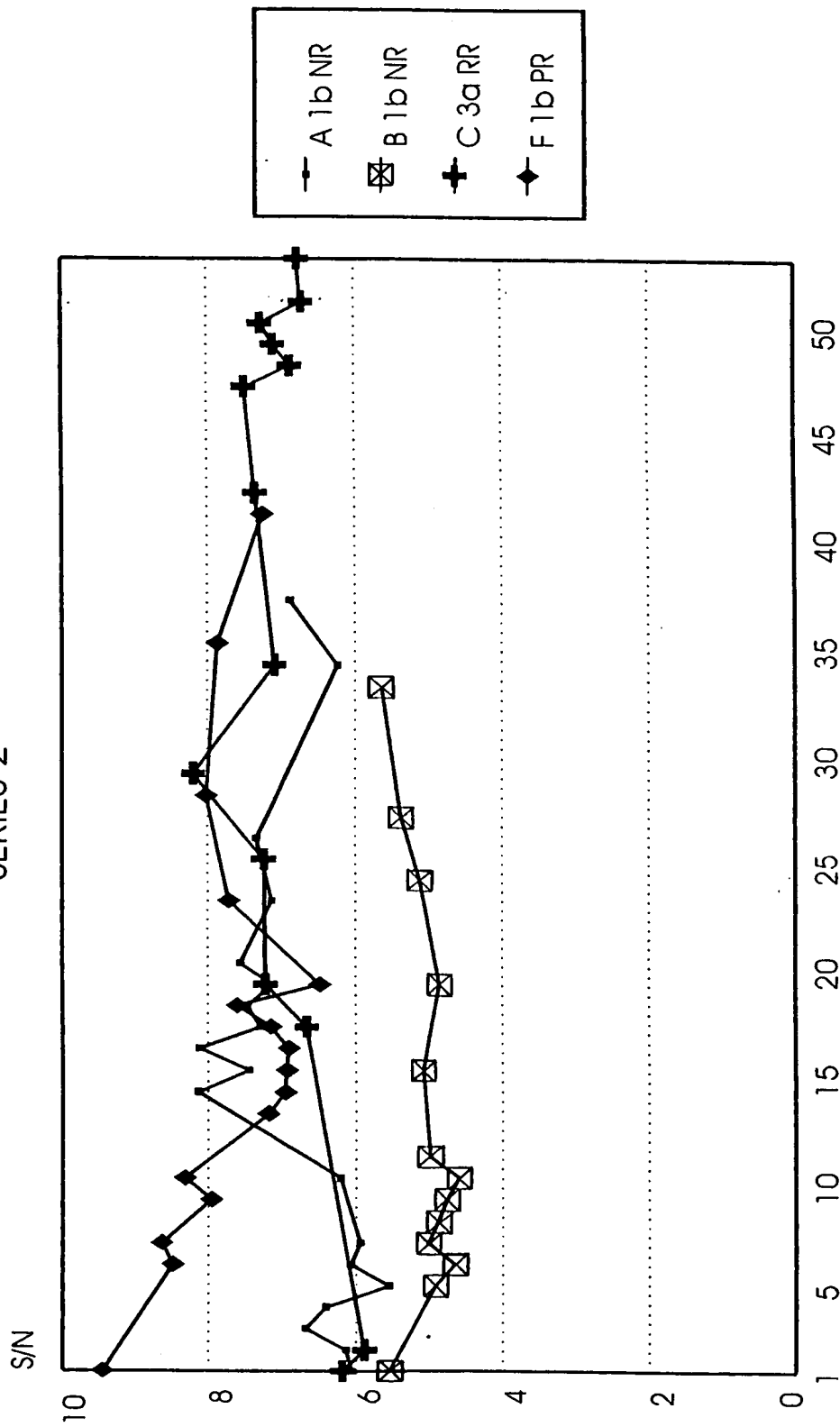


weeks after start of treatment

Fig.10

Anti-E2 levels in INCOMPLETE responders to IFN treatment

SERIES 2

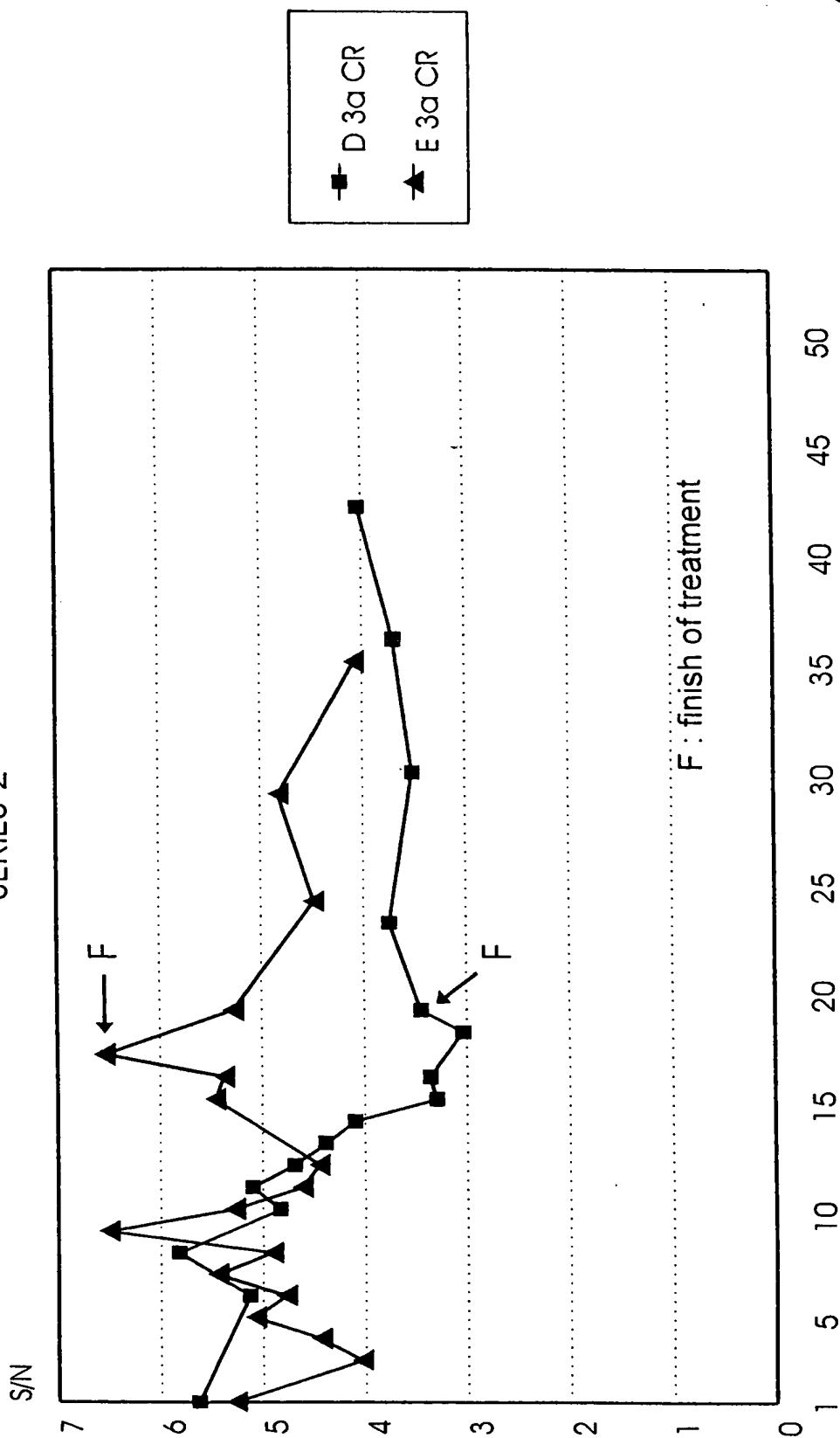


months after start of treatment

Fig.11

Anti-E2 levels in COMPLETE responders to IFN treatment

SERIES 2



months after start of treatment

Fig.12



Human anti-E1 reactivity competed with peptides

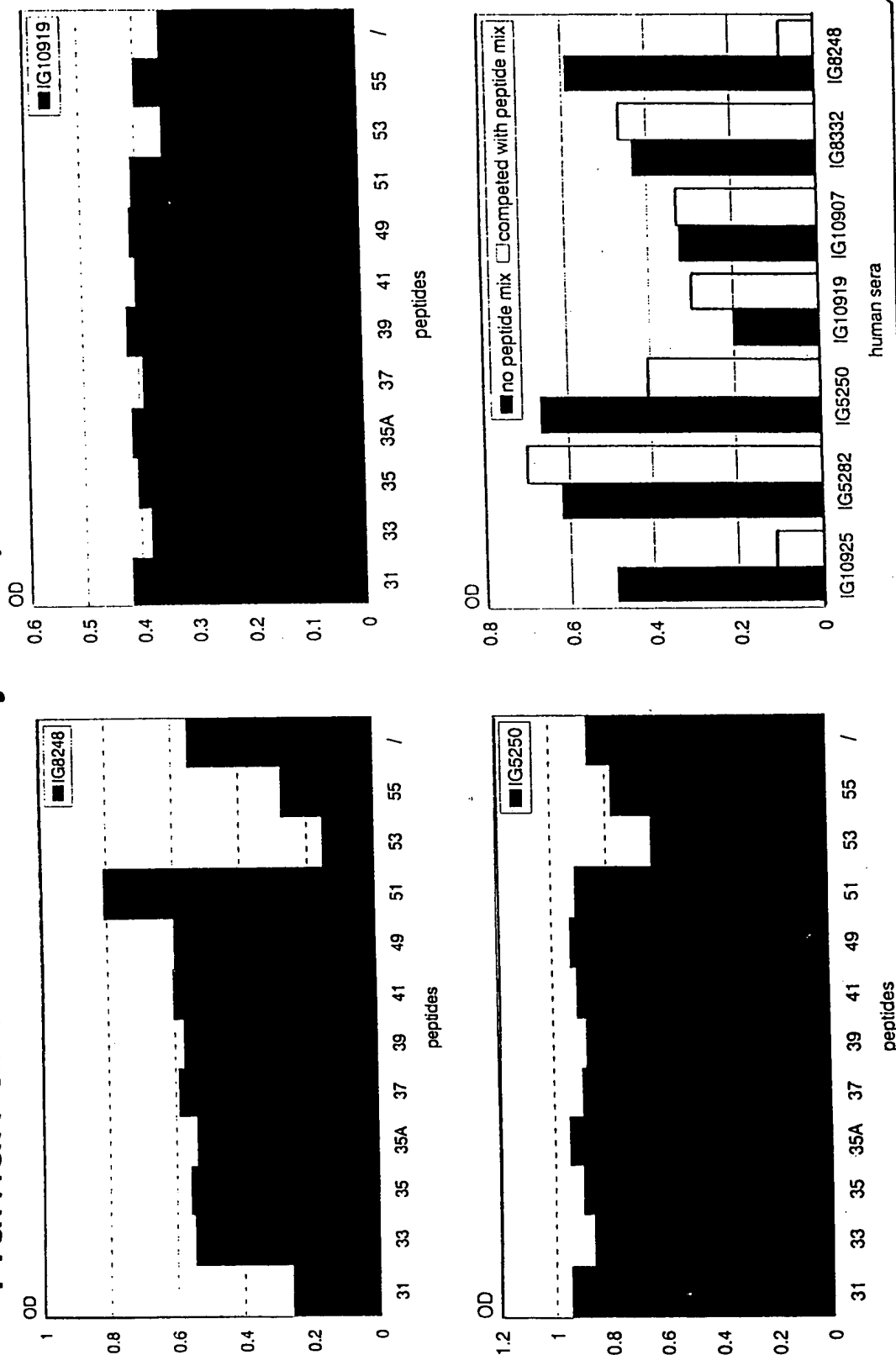


Fig.13

Competition of reactivity of anti-E1 Mabs with peptides

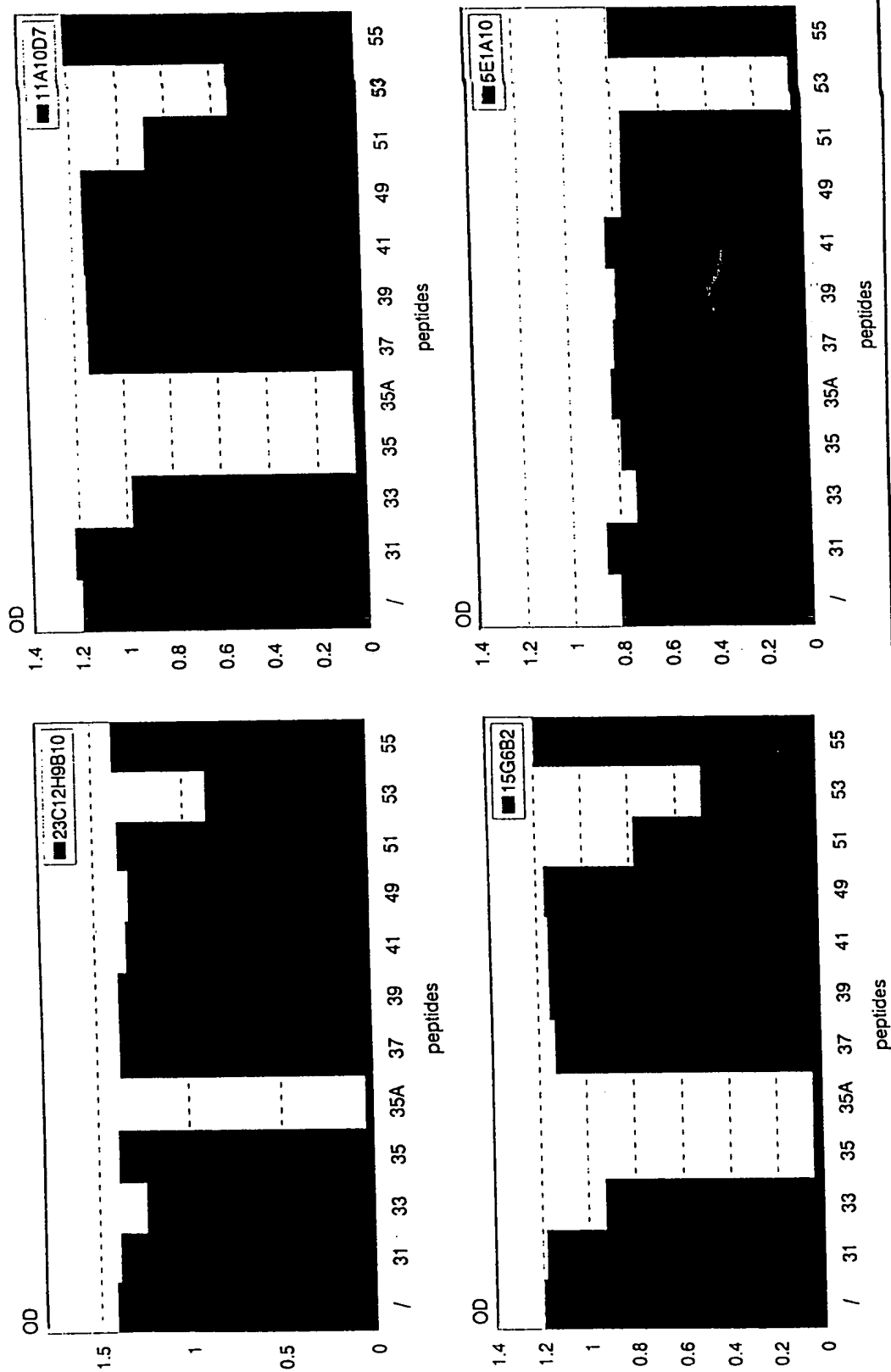


Fig.14

Anti-E1 (epitope 1) levels in NON-RESPONDERS to IFN treatment

SERIES 1

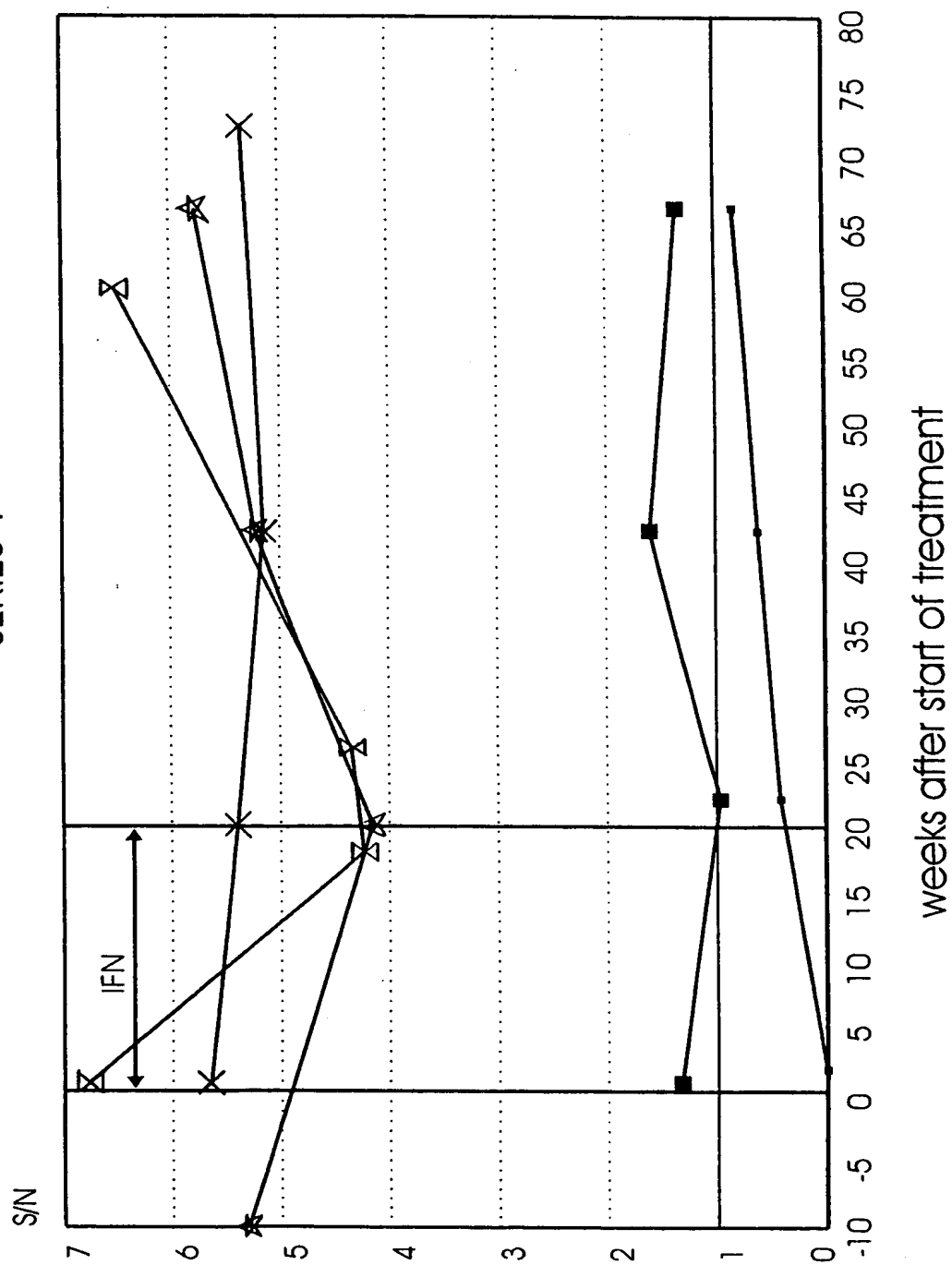
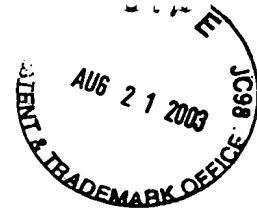


Fig.15



Anti-E1 (epitope 1) levels in RESPONDERS to IFN treatment

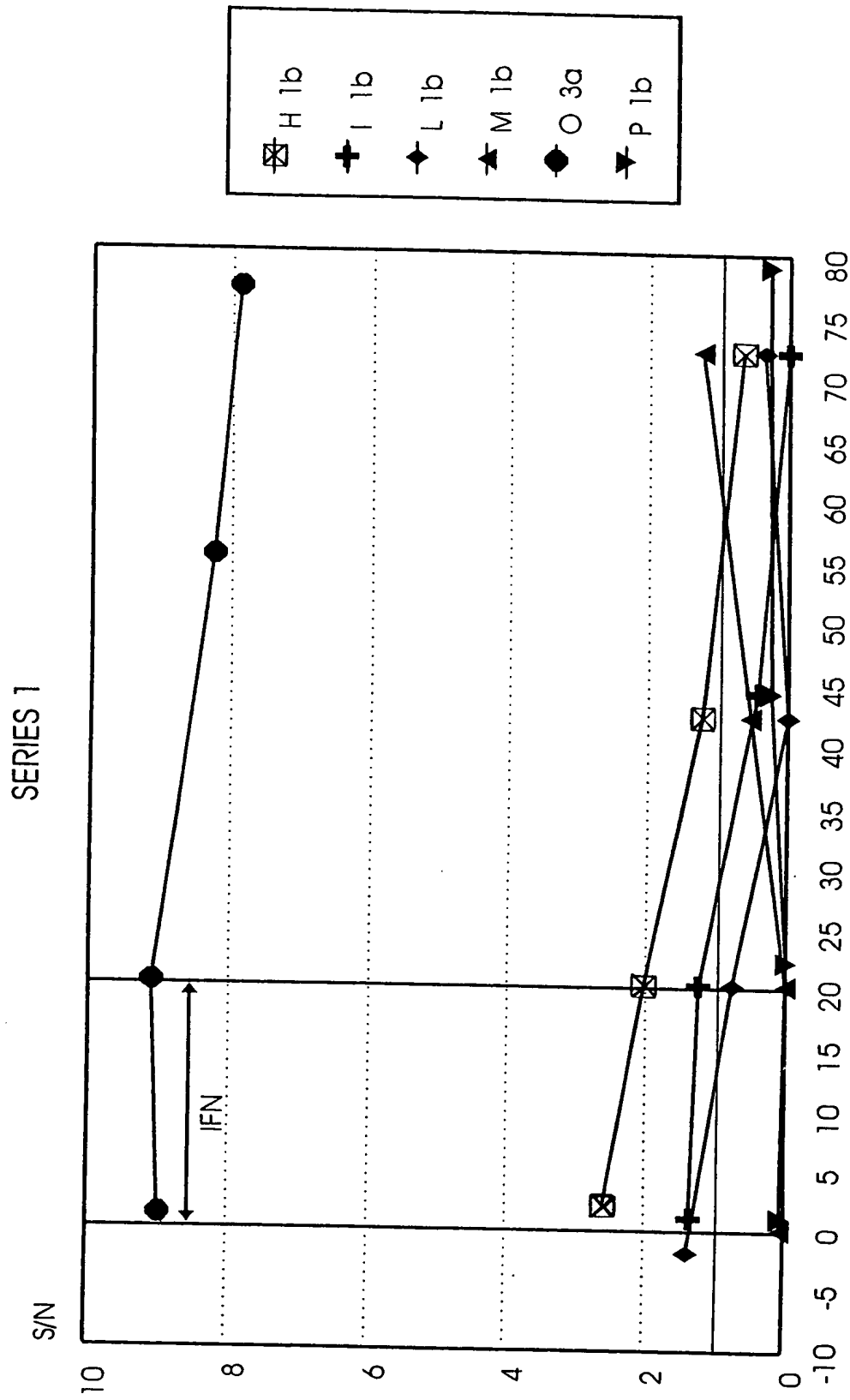
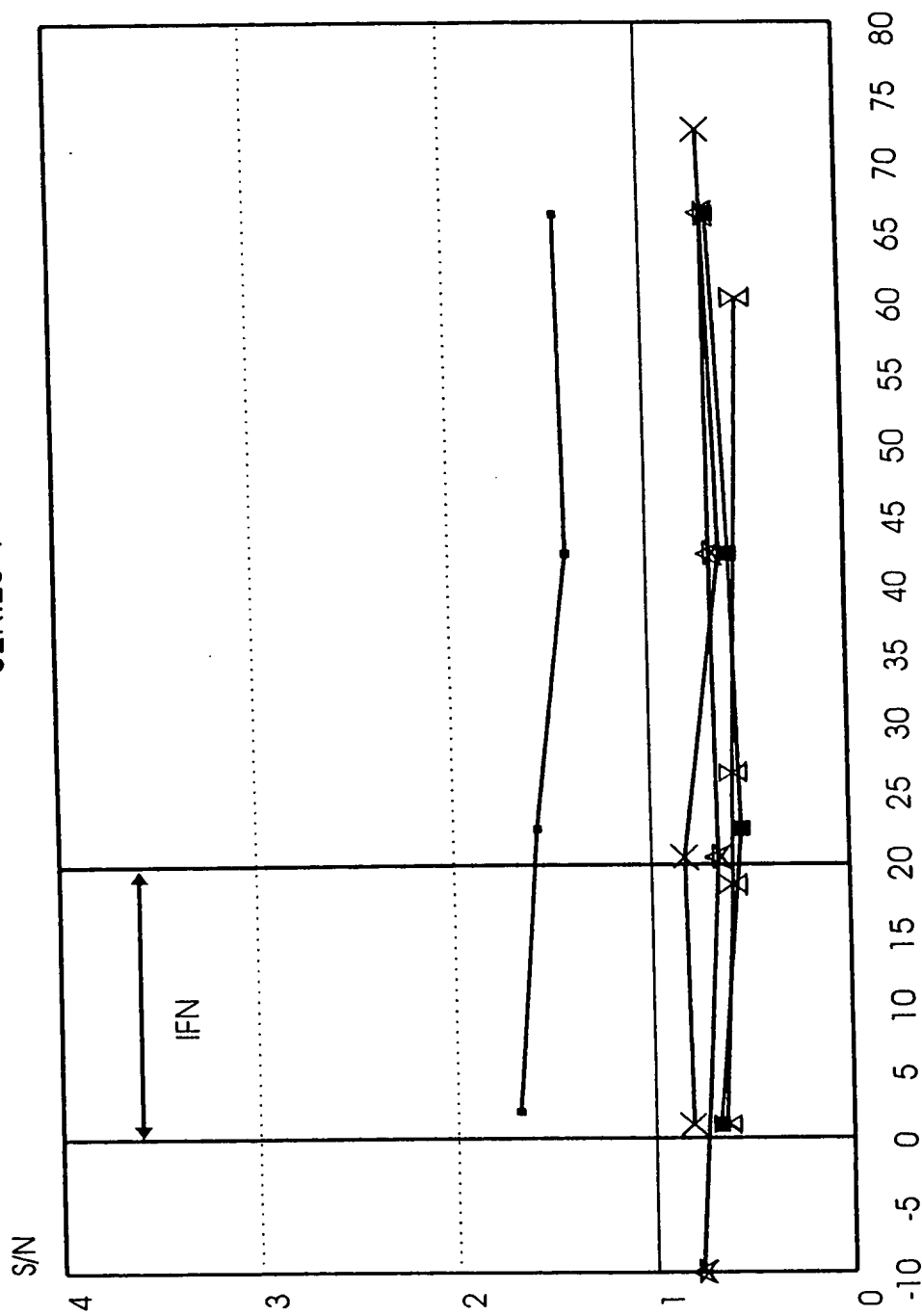


Fig.16

Anti-E1 (epitope 2) levels in NON-RESPONDERS to IFN treatment

SERIES 1

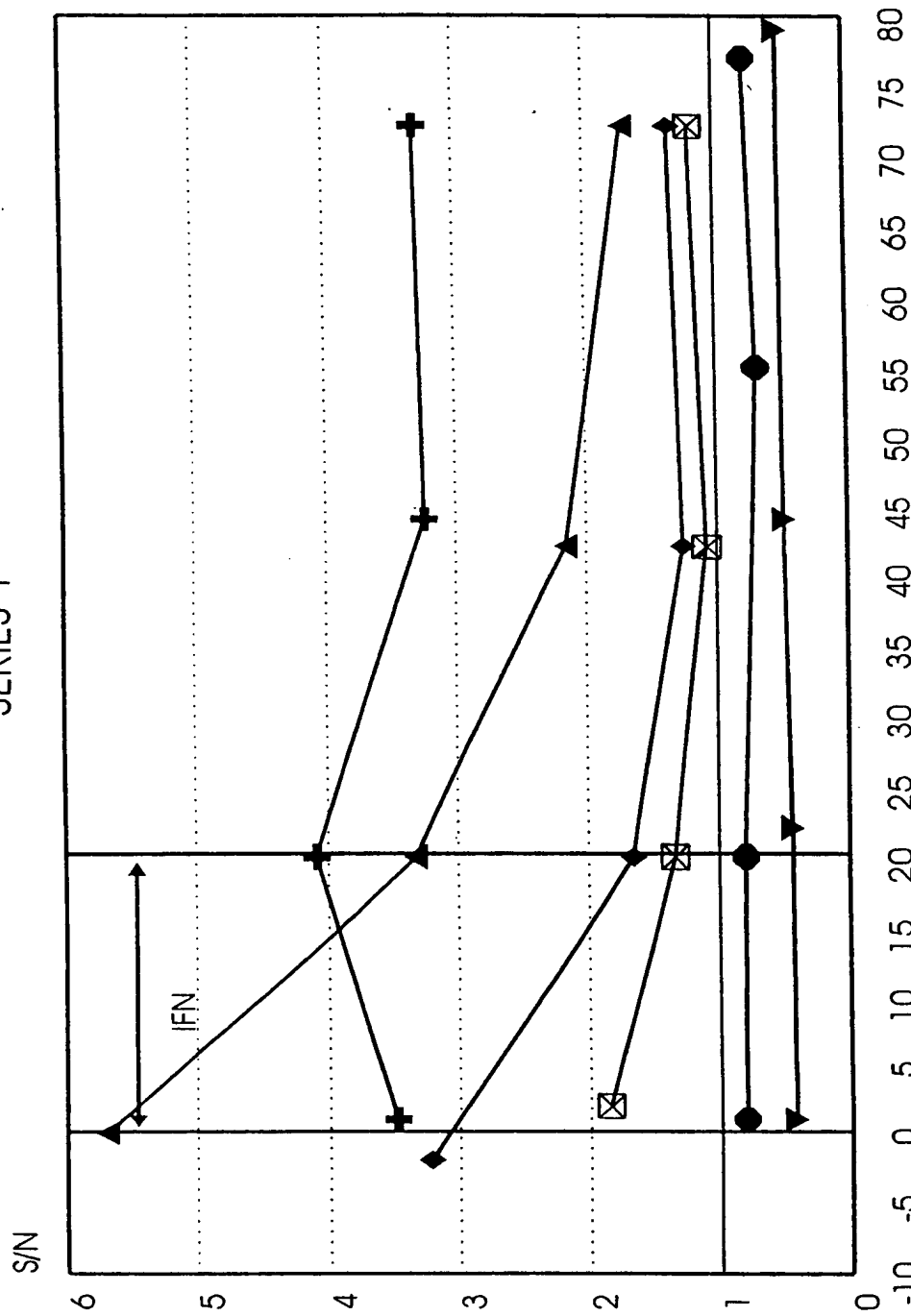


weeks after start of treatment

Fig.17

Anti-E1 (epitope 2) levels in RESPONDERS to IFN treatment

SERIES 1



weeks after start of treatment

Fig.18

Competition of reactivity of anti-E2 Mabs with peptides

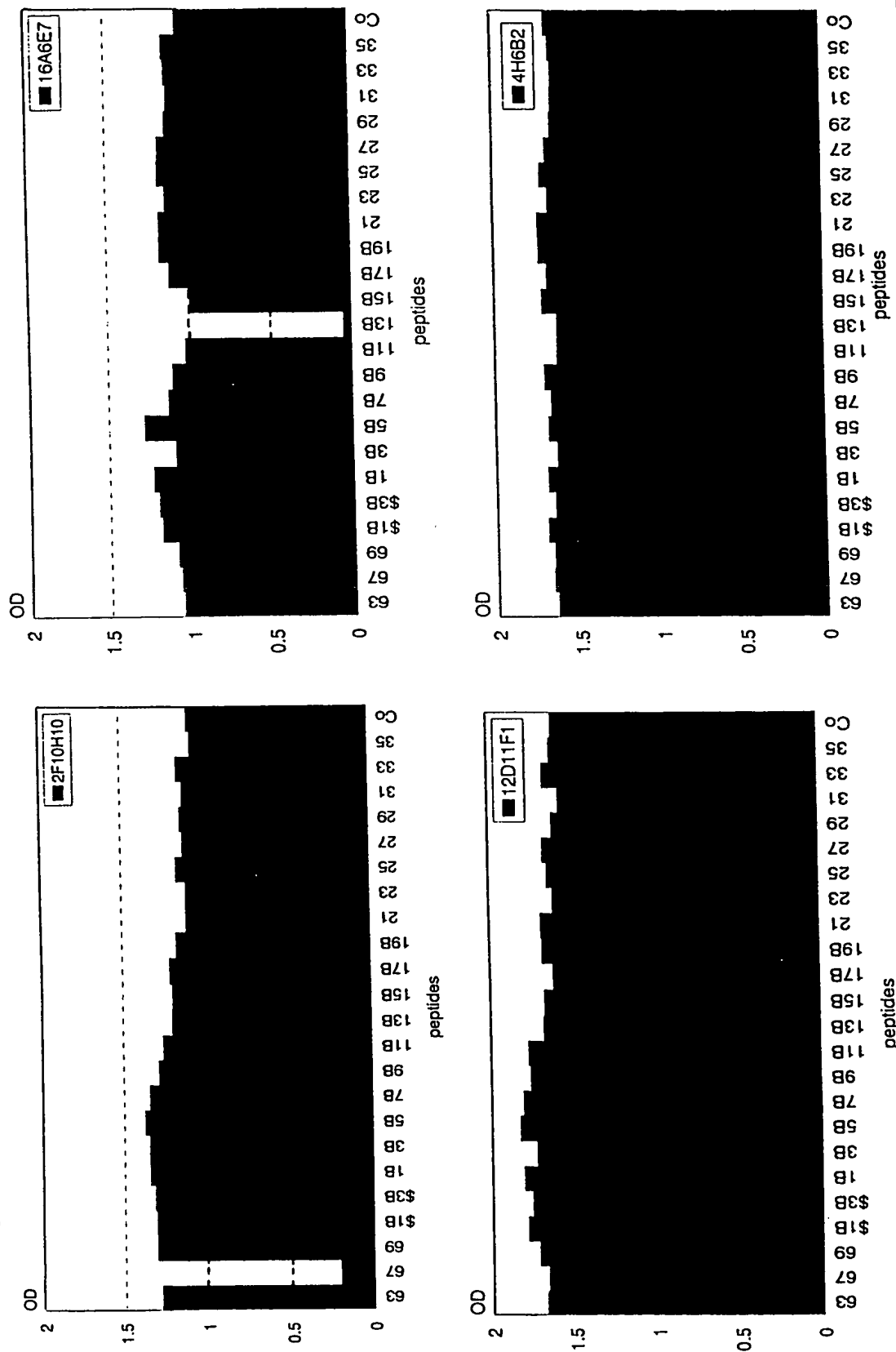


Fig.19

Human anti-E2 reactivity competed with peptides

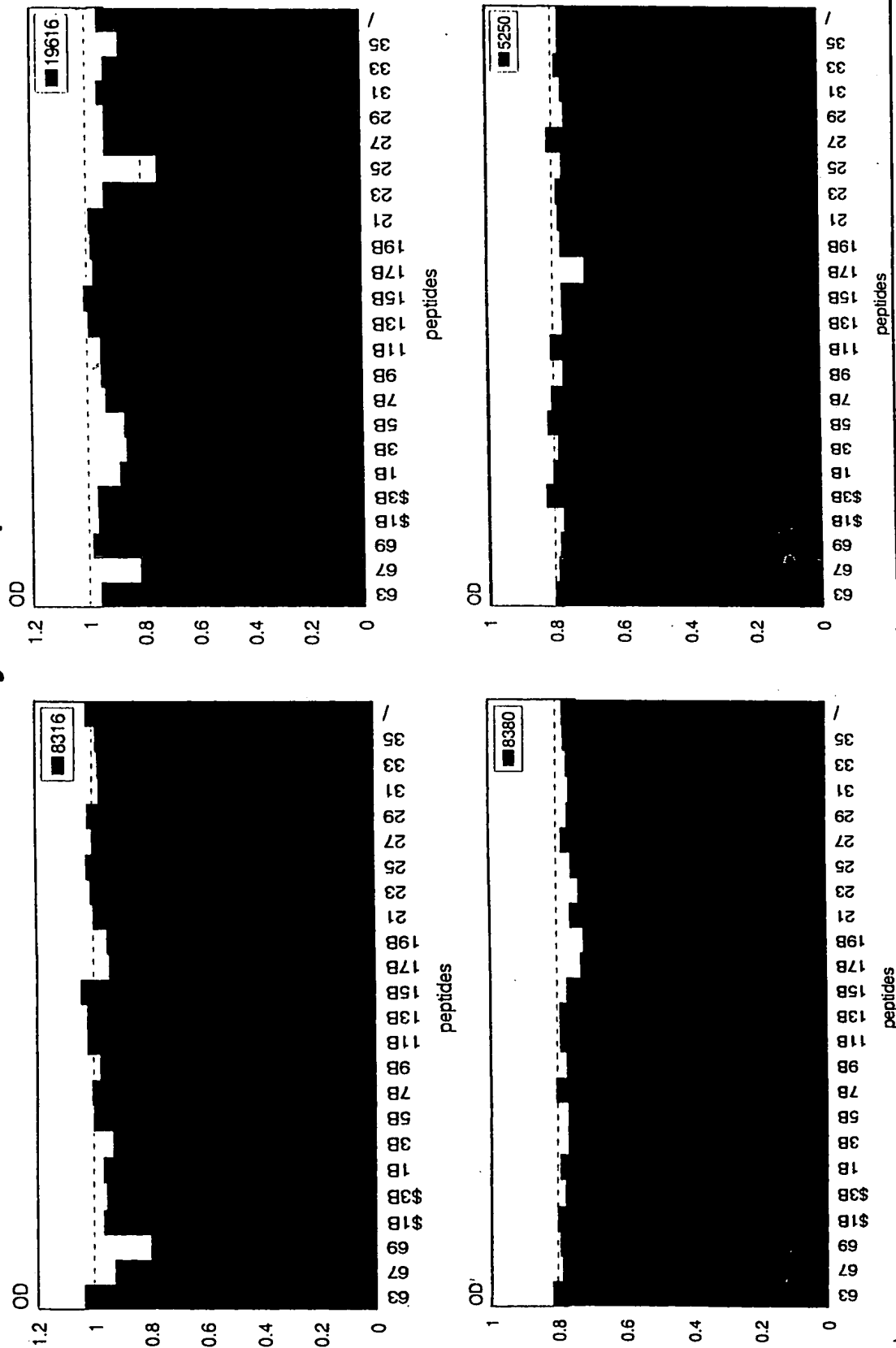


Fig. 20



Fig. 21A

5' GGCATGCAAGCTTAATTAATT3' (SEQ ID NO 1)

3'ACGTCCGTACGTTCTGAATTAATTAATCGA5' (SEQ ID NO 94)

5'CCGGGGAGGCCTGCACGTGATCGAGGGCAGACACCATCACCACCATCACTAATAGT
TAATTAAGTCA 3' (SEQ ID NO 2)

3'CCTCCGGACGTGCACTAGCTCCCGTCTGTGGTAGTGGTGGTAGTGATTATCAATTAATTG
5' (SEQ ID NO 95)

SEQ ID NO 3 (HCCI9A)

ATGCCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTACTGTCCTGTCTGACCATTCCA
GCTTCCGCTTATGAGGTGCGCAACGTGTCCGGGATGTACCATGTACGAACGACTGCT
CCAACTCAAGCATTGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGT
GCCCTGCGTTCCGGGAGAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTC
GCAGCTAGGAACGCCAGCGTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCG
TTGGGGCGGGCTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTC
CTCGTCTCCAGCTGTTACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCA
ATTGCTCAATCTATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGAT
GAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCT
GTCGTGGACATGGTGGCGGGGGCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATT
CCATGGTGGGGAAGTGGGCTAAGGTTTTGATTGTGATGCTACTCTTTGCTCTCTAATAG

SEQ ID NO 5 (HCCI10A)

ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT
ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGGCTGCTTTCTG



Fig. 21B

TTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCA
CCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGG
CCACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTACAACG
GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGG
GGGCCCATTTGGGGAGTCTGGCGGGTCTCGCCTACTATTCCATGGTGGGGAACTGGGC
TAAGGTTTTGATTGTGATGCTACTCTTTGCTCCCTAATAG

SEQ ID NO 7 (HCCI11A)

ATGTTGGGTAAGGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTCCG
GTTTCTGGAAGACGGCGTGAACATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTA
TCTTCCTCTTGGCTTTACTGTCCTGTCTGACCATTCCAGCTTCCGCTTATGAGGTGCGC
AACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACCTCAAGCATTGTGTATG
AGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCCGGGAGAACA
ACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGT
CCCCACTACGACAATACGACGCCACGTGATTTGCTCGTTGGGGCGGCTGCTTTCTGTT
CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTACCC
ATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCC
ACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTAATAG

SEQ ID NO 9 (HCCI12A)

ATGCCCGTTGCTCTTTCTCTATCTTCCTCTTGGCCCTGCTGTCCTGTCTGACCATACCA
GCTTCCGCTTATGAAGTGCGCAACGTGTCCGGGGTGTTACCATGTCACGAACGACTGCT
CCAACCTCAAGCATAGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGT
GCCCTGCGTTCCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTC
GCGGCCAGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTGATTTGCTC
GTTGGGGCTGCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTT
CCTTGTTTCCCAGCTGTTACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCA
ACTGCTCAATCTATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAT
GAACTGGTCCTAATAG

SEQ ID NO 11 (HCCI13A)

ATGTCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCCCTGCTGTCCTGTCTGACCATACCA
GCTTCCGCTTATGAAGTGCGCAACGTGTCCGGGGTGTTACCATGTCACGAACGACTGCT
CCAACCTCAAGCATAGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGT



Fig. 21C

GCCCTGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTC
GCGGCCAGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTC
GTTGGGGGCTGCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTT
CCTTGTTTCCCAGCTGTTACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCA
ACTGCTCAATCTATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAT
GAACTGGTAATAG

SEQ ID NO 13 (HCCI17A)

ATGCTGGGTAAGGCCATCGATACCCTTACGTGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAAGACGGCGTGAACATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTA
TCTTCCTCTTGGCTTTACTGTCCTGTCTAACCATTCCAGCTTCCGCTTACGAGGTGCGC
AACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTATG
AGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACA
ACTCTTCCCGCTGCTGGGTAGCGCTACCCCCACGCTCGCGGCTAGGAACGCCAGCAT
CCCCACTACAACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTT
CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTACC
ATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCC
ACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTACTAATAG

SEQ ID NO 15 (HCPPr51)

ATGCCCGGTTGCTCTTTCTCTATCTT

SEQ ID NO 16 (HCPPr52)

ATGTTGGGTAAGGTCATCGATACCCT

SEQ ID NO 17 (HCPPr53)

CTATTAGGACCAGTTCATCATCATATCCCA

SEQ ID NO 18 (HCPPr54)

CTATTACCAGTTCATCATCATATCCCA

SEQ ID NO 19 (HCPPr107)

ATACGACGCCACGTCGATTCCCAGCTGTTACCATC



Fig. 21D

SEQ ID NO 20 (HCP108)

GATGGTGAACAGCTGGGAATCGACGTGGCGTCGTAT

SEQ ID NO 21 (HCCI37)

ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT
ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTGATTCCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTAT
CGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCATTGGGG
AGTCCTGGCGGGTCTCGCCTACTATTCCATGGTGGGGAACCTGGGCTAAGGTTTTGATTG
TGATGCTACTCTTTGCTCCCTAATAG

SEQ ID NO 23 (HCCI38)

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TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT
ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTGATTCCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGATGAACTGGTAA
TAG

SEQ ID NO 25 (HCCI39)

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TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT



Fig. 21E

ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTGATTCCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTAT
CGCAGCTGCTCCGGATCCTCTAATAG

SEQ ID NO 27 (HCCI40)

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GGTTCTGGAGGACGGCGTGAACATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT
ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTGATTCCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTAT
CGCAGCTGCTCCGGATCGTGATCGAGGGCAGACACCATCACCACCATCACTAATAG

SEQ ID NO 29 (HCCI62)

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CGCTCGTCGGCGCTCCCGTAGGAGGCGTCGCAAGAGCCCTTGCGCATGGCGTGAGGGC
CCTTGAAGACGGGATAAATTTGCAACAGGGAATTTGCCCGGTTGCTCCTTTTCTATTT
TCCTTCTCGCTCTGTTCTCTTGCTTAATTCATCCAGCAGCTAGTCTAGAGTGGCGGAAT
ACGTCTGGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGTATTGTGTACGAGGC
CGATGACGTTATTCTGCACACACCCGGCTGCATACCTTGTGTCCAGGACGGCAATACA
TCCACGTGCTGGACCCCAGTGACACCTACAGTGGCAGTCAAGTACGTCGGAGCAACCA
CCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGATGTGCTCTGC
GCTCTACGTGGGTGACATGTGTGGGGCTGTCTTCCTCGTGGGACAAGCCTTCACGTTCA
GACCTCGTCGCCATCAAACGGTCCAGACCTGTAACCTGCTCGCTGTACCCAGGCCATCT
TTCAGGACATCGAATGGCTTGGGATATGATGATGAACTGGTAATAG



Fig. 21F

SEQ ID NO 31 (HCCI63)

ATGGGTAAGGTCATCGATACCCTAACGTGCGGATTCGCCGATCTCATGGGGTATATCC
CGCTCGTAGGCGGGCCCCATTGGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGT
CCTTGAGGACGGGGTAAACTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCT
TTATTCTTGCTCTTCTCTCGTGTCTGACCGTTCCGGCCTCTGCAGTTCCTACCGAAATG
CCTCTGGGATTTATCATGTTACCAATGATTGCCCAAACCTCTTCCATAGTCTATGAGGCA
GATAACCTGATCCTACACGCACCTGGTTGCGTGCCTTGTGTCATGACAGGTAATGTGA
GTAGATGCTGGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTCGGAGCAGTCAC
GGCTCCTCTTCGGAGAGCCGTTGACTACCTAGCGGGAGGGGCTGCCCTCTGCTCCGCG
TTATACGTAGGAGACGCGTGTGGGGCACTATTCTTGGTAGGCCAAATGTTACCTATA
GGCCTCGCCAGCACGCTACGGTGCAGAACTGCAACTGTTCCATTTACAGTGGCCATGT
TACCGGCCACCGGATGGCATGGGATATGATGATGAACTGGTAATAG

SEQ ID NO 33 (HCP109)

TGGGATATGATGATGAACTGGTC

SEQ ID NO 34 (HCP72)

CTATTATGGTGGTAAKGCCARCARGAGCAGGAG

SEQ ID NO 35 (HCCL22A)

TGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCC
GGATCCCACAAGCTGTCTGTTGACATGGTGGCGGGGGGCCATTGGGGAGTCCTGGCGG
GCCTCGCCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTTTTGGTTGTGATGCTACTC
TTTGCCGGCGTCGACGGGCATACCCGCGTGTGAGGAGGGGCGAGCAGCCTCCGATACCA
GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACAC
CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAAC
AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAG
CGCTTGGCCAGCTGTCTGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTT
ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC
GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC
CTGTTGTGGTGGGGACGACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAA
CGACTCGGATGTGCTGATTCTCAACAACACGCGGCCGCGCGAGGCAACTGGTTCGGC
TGTACATGGATGAATGGCACTGGGTTCACCAAGACGTGTGGGGGGCCCCCGTGCAACA
TCGGGGGGGGCCGGCAACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCC
CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT

Fig. 21G

CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCTGAAGCCGCATGCAATTGGACTCG
AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG
TCTACAACAGAGTGGCAGATACTGCCCTGTTCTTCACCACCCTGCCGGCCCTATCCA
CCGGCCTGATCCACCTCCATCAGAACATCGTGGACGTGCAATACCTGTACGGTGTAGG
GTCGGCGGTTGTCTCCCTTGTCAATGGGAGTATGTCCTGTTGCTCTTCCTTCTCCT
GGCAGACGCGCGCATCTGCGCCTGCTTATGGATGATGCTGCTGATAGCTCAAGCTGAG
GCCGCCTTAGAGAACCTGGTGGTCCTCAATGCGGCGGCCGTGGCCGGGGCGCATGGC
ACTCTTTCCTTCTTGTGTTCTTCTGTGCTGCCTGGTACATCAAGGGCAGGCTGGTCCC
TGGTGCGGCATACGCCTTCTATGGCGTGTGGCCGCTGCTCCTGCTTCTGCTGGCCTTAC
CACCACGAGCTTATGCCTAGTAA

SEQ ID NO 37 (HCCI41)

GATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGGCCATTGGGGAGTCCTGGCGGG
CCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCT
TTGCCGGCGTCGACGGGCATACCCGCGTGTGAGGAGGGGCAGCAGCCTCCGATACCA
GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTGCGCTCAGAAAATCCAGCTCGTAAACAC
CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAAC
AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAG
CGTTGGCCAGCTGTGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTT
AACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC
GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC
CTGTTGTGGTGGGGACGACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAA
CGACTCGGATGTGCTGATTCTCAACAACACGCGGCCGCGCGAGGCAACTGGTTCGGC
TGTACATGGATGAATGGCACTGGGTTACCAAGACGTGTGGGGGGCCCCCGTGCAACA
TCGGGGGGGGCCGGCAACAACACCTTGACCTGCCCCACTGACTGTTTTTCGGAAGCACCC
CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT
CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCTGAAGCCGCATGCAATTGGACTCG
AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG
TCTACAACAGAGTGGCAGAGTGGCAGAGCTTAATTAATTAG

SEQ ID NO 39 (HCCI42)

GATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGGCCATTGGGGAGTCCTGGCGGG
CCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCT



Fig. 21H

TTGCCGGCGTCGACGGGCATACCCGCGTGTTCAGGAGGGGCAGCAGCCTCCGATACCA
GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACAC
CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAAC
AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAG
CGCTTGGCCAGCTGTGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTT
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GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC
CTGTTGTGGTGGGGACGACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAA
CGACTCGGATGTGCTGATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGC
TGTACATGGATGAATGGCACTGGGTTACCAAGACGTGTGGGGGGCCCCCGTGCAACA
TCGGGGGGGGCCGGCAACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCC
CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGT
CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCTGAAGCCGCATGCAATTGGACTCG
AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG
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SEQ ID NO 41 (HCCI43)

ATGGTGGGGAACCTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACG
GGCATACCCGCGTGTTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCT
CTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC
ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC
TATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTGCG
CTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTTAACTGAGCCTAACAGC
TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG
CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC
GACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTG
ATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATG
GCACTGGGTTACCAAGACGTGTGGGGGGCCCCCGTGCAACATCGGGGGGGCCGGCA
ACAACACCTTGACCTGCCCCACTGACTGTTTTTCGGAAGCACCCCGAGGCCACCTACGC
CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGG
CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGG
GGGCGTGGAGCACAGGTTCTGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGA
CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGG
CAGAGCTTAATTAATTAG



Fig. 21I

SEQ ID NO 43 (HCCI44)

ATGGTGGGGAAGTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACG
GGCATACCCGCGTGTGAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCT
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SEQ ID NO 45 (HCCL64)

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Fig. 21J

TGGAGCACAGGTTCTGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGA
GGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATA
CTGCCCTGTTCTTCACCACCCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCA
GAACATCGTGGACGTGCAATACCTGTACGGTGTAGGGTCGGCGGTTGTCTCCCTTGTC
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CTGCTTATGGATGATGCTGCTGATAGCTCAAGCTGAGGCCGCCTTAGAGAACCTGGTG
GTCCTCAATGCGGCGGCCGTGGCCGGGGCGCATGGCACTCTTTCCTTCCTTGTGTTCTT
CTGTGCTGCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGCGGCATACGCCTTCTAT
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SEQ ID NO 47 (HCCI65)

AATTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT
ATCTTCCTCTTGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTGATTTGCTCGTTGGGGCGGCTGCTTTCTG
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CCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGG
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GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTGCTGGACATGGTGGCGG
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CTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGT
CCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGACGACCGATCGGTTTGGTGT
CCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTCAACAACACGCGG
CCGCCGCGAGGCAACTGGTTTCGGCTGTACATGGATGAATGGCACTGGGTTACCAAGA
CGTGTGGGGGCCCCCGTGCAACATCGGGGGGGCCGGCAACAACACCTTGACCTGCC

Fig. 21K

CCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTCTGGGCC
CTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGGCACTACCCCTGCA
CTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGGGGGCGTGGAGCACAGGTT
CGAAGCCGCATGCAATTGGA CTGAGGAGAGCGTTGTGACTTGGAGGACAGGGATAG
ATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATACTGCCCTGTTCC
TTCACCACCCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCAGAACATCGTGG
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GTATGTCTGTTGCTCTTCCTTCTCCTGGCAGACGCGCGCATCTGCGCCTGCTTATGGA
TGATGCTGCTGATAGCTCAAGCTGAGGCCGCCTTAGAGAACCTGGTGGTCCTCAATGC
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GGTACATCAAGGGCAGGCTGGTCCCTGGTGCGGCATAACGCTTCTATGGCGTGTGGCC
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SEQ ID NO 49 (HCCI66)

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GCAGGGGCCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAAC
CTCGTGGGAGGGCGACAACCTATCCCCAAGGCTCGCCGACCCGAGGGTAGGGCCTGGG
CTCAGCCCGGGTACCCTTGGCCCCTCTATGGCAATGAGGGCATGGGGTGGGCAGGATG
GCTCCTGTACCCCCGCGGCTCTCGGCCTAGTTGGGGCCCTACAGACCCCCGGCGTAGG
TCGCGTAATTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGG
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CGTCCGGGTTCTGGAGGACGGCGTGAACCTATGCAACAGGGAATTTGCCCGGTTGCTCT
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AGCGTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTT
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Fig. 21L

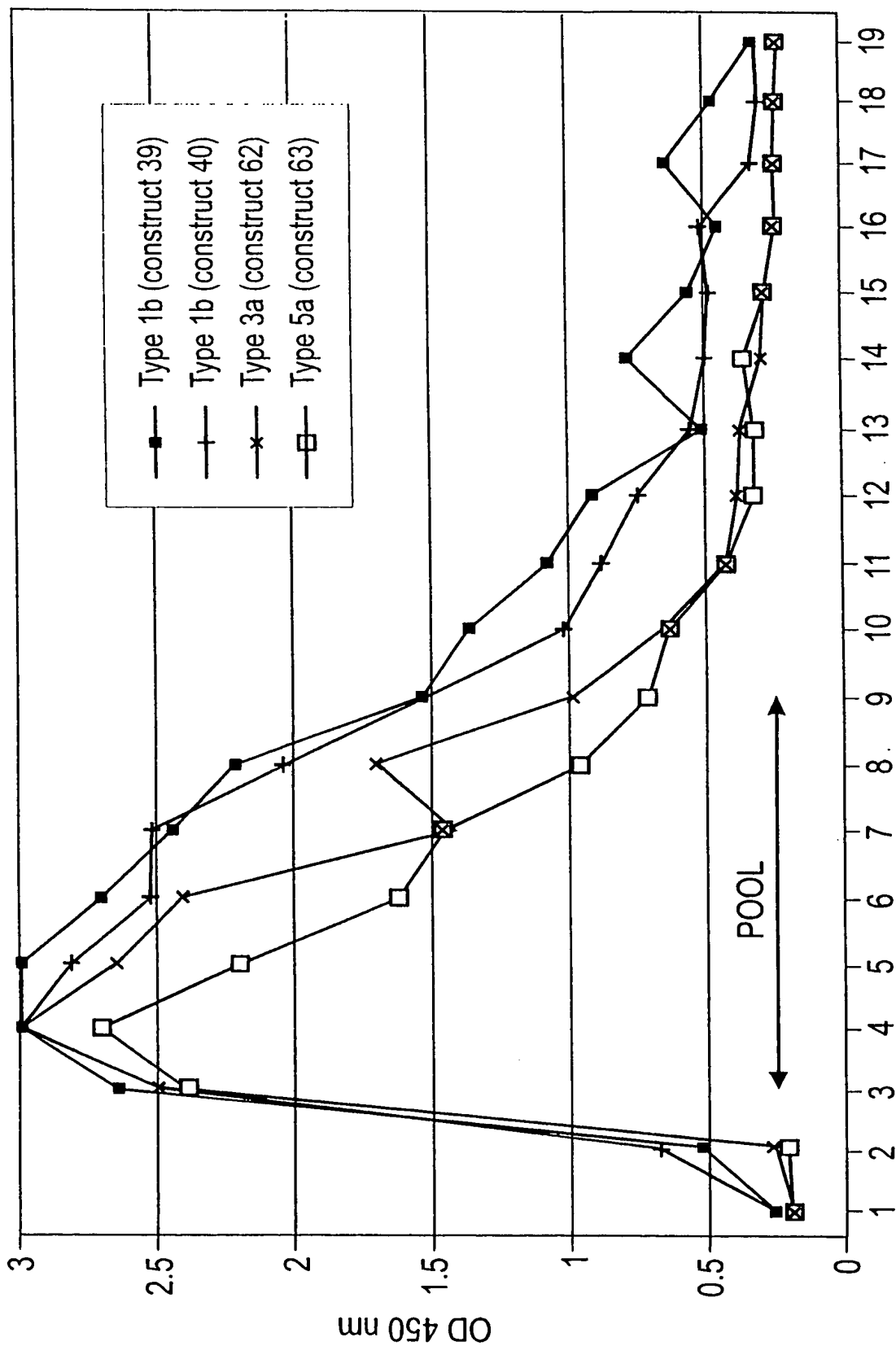
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GCTGCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGCGGCATAACGCTTCTATGGCG
TGTGGCCGCTGCTCCTGCTTCTGCTGGCCTTACCACCACGAGCTTATGCCTAGTAA



Fig. 22

OD measured at 450 nm
construct

Fraction	volume	dilution	39 Type 1b	40 Type 1b	62 Type 3a	63 Type 5a
START	23 ml	1/20	2.517	1.954	1.426	1.142
FLOW THROUGH	23 ml	1/20	0.087	0.085	0.176	0.120
1	0.4 ml	1/200	0.102	0.051	0.048	0.050
2			0.396	0.550	0.090	0.067
3			2.627	2.603	2.481	2.372
4			3	2.967	3	2.694
5			3	2.810	2.640	2.154
6			2.694	2.499	1.359	1.561
7			2.408	2.481	0.347	1.390
8			2.176	1.970	1.624	0.865
9			1.461	1.422	0.887	0.604
10			1.286	0.926	0.543	0.519
11			0.981	0.781	0.294	0.294
12			0.812	0.650	0.249	0.199
13			0.373	0.432	0.239	0.209
14			0.653	0.371	0.145	0.184
15			0.441	0.348	0.151	0.151
16			0.321	0.374	0.098	0.106
17			0.525	0.186	0.099	0.108
18			0.351	0.171	0.083	0.090
19			0.192	0.164	0.084	0.087



FRACTIES

Fig. 23

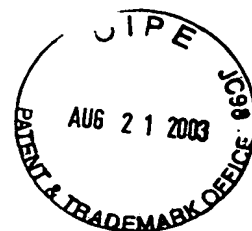


Fig. 24

Fraction	volume	dilution	OD measured at 450 nm			
			construct			
			39 Type 1b	40 Type 1b	62 Type 3a	63 Type 5a
20	250 μ l	1/200	0.072	0.130	0.096	0.051
21			0.109	0.293	0.084	0.052
22			0.279	0.249	0.172	0.052
23			0.093	0.151	0.297	0.054
24			0.080	0.266	0.438	0.056
25			0.251	0.100	0.457	0.048
26			3	1.649	0.722	0.066
27			3	3	2.528	0.889
28			3	3	3	2.345
29			3	3	2.849	2.580
30			2.227	1.921	1.424	1.333
31			0.263	0.415	0.356	0.162
32			0.071	0.172	0.154	0.064
33			0.103	0.054	0.096	0.057
34			0.045	0.045	0.044	0.051
35			0.043	0.047	0.045	0.046
36			0.045	0.045	0.049	0.040
37			0.045	0.047	0.046	0.048
38			0.046	0.048	0.047	0.057
39			0.045	0.048	0.050	0.057
40			0.046	0.049	0.048	0.049

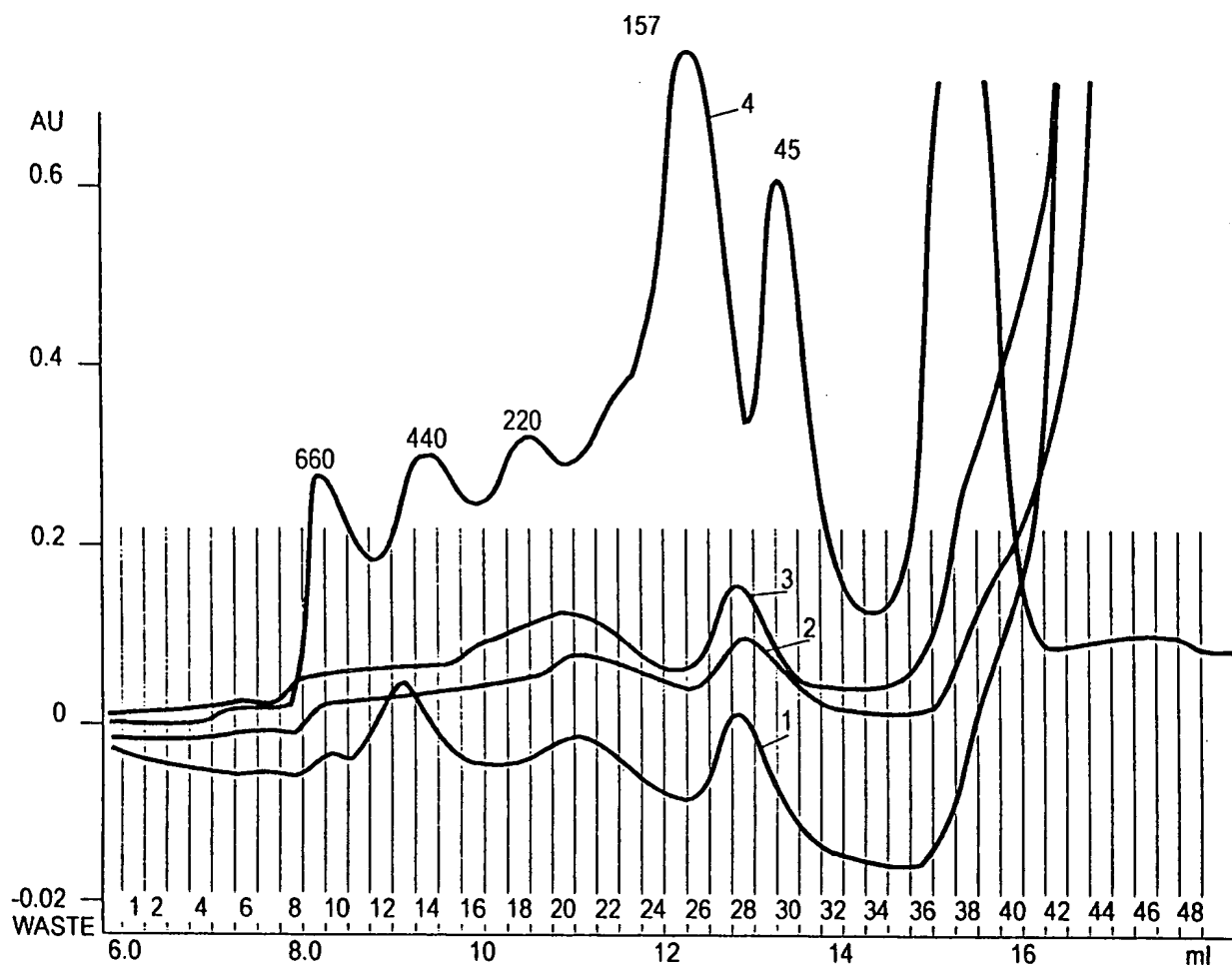


Fig. 25

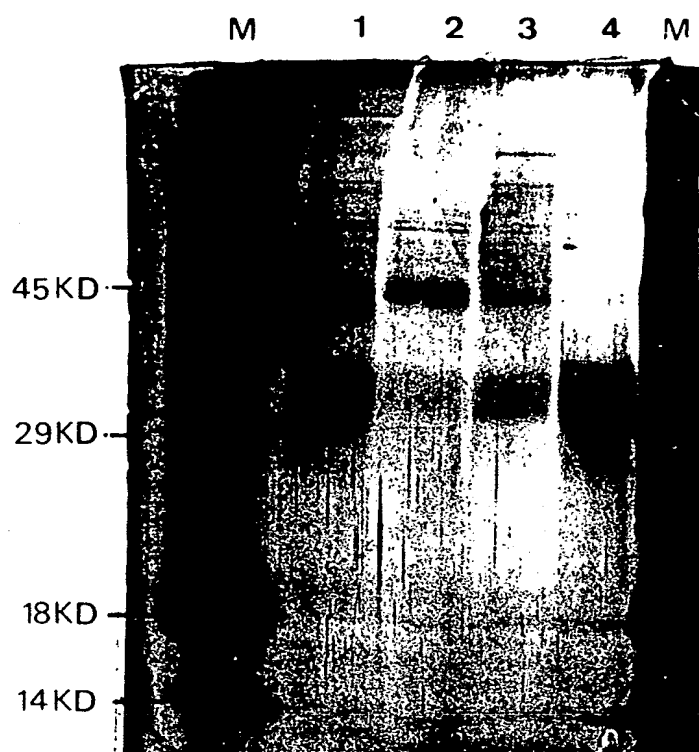


Fig. 26

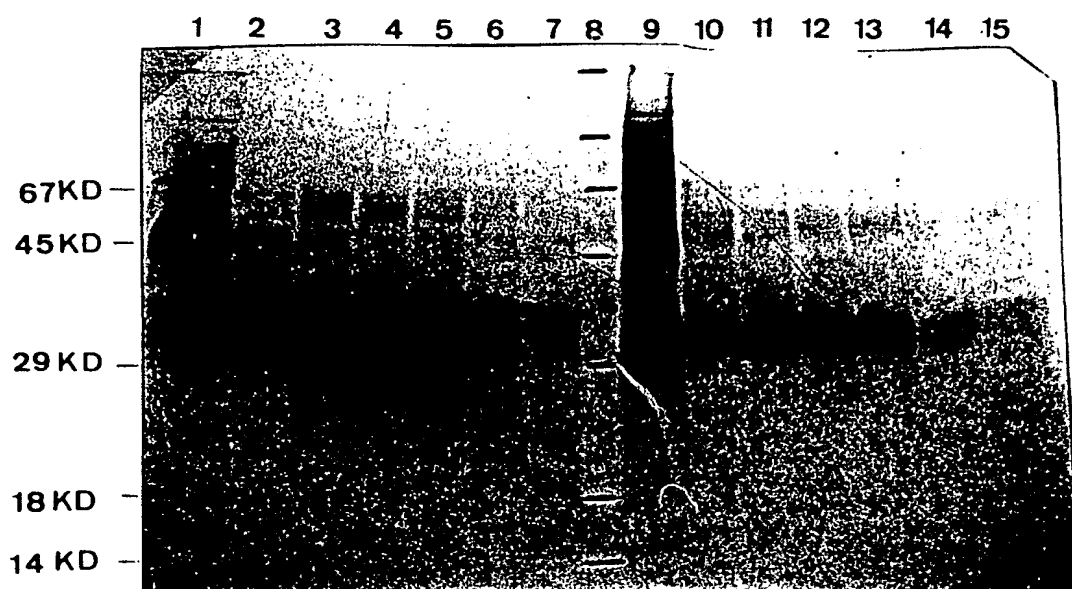


Fig. 27

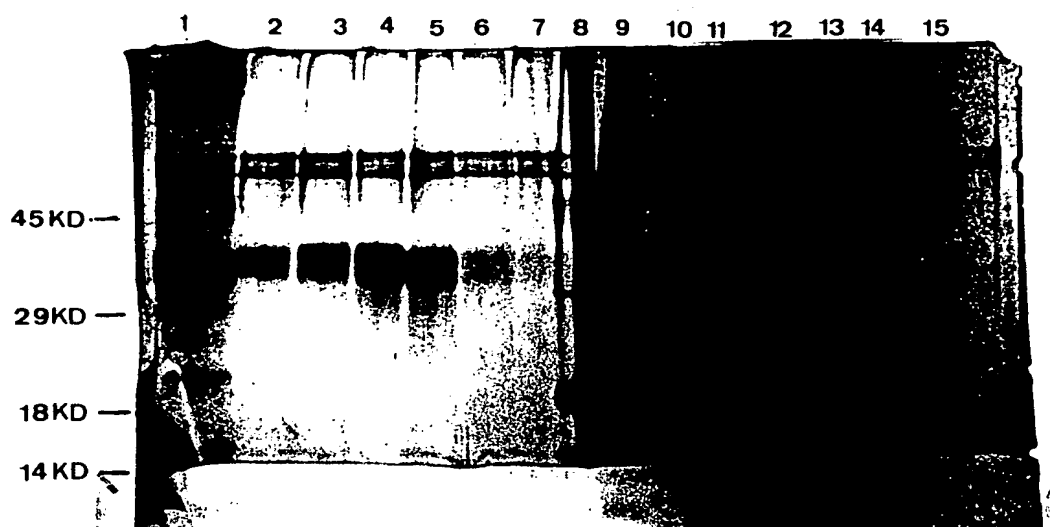


Fig.28

M 1 2 3 4 5 6

67 kD -

45 kD -

29 kD -

18 kD -

14 kD -

Lane 1: Crude Lysate
 Lane 2: Flow through Lentil Chromatography
 Lane 3: Wash with EMPIGEN Lentil Chromatography
 Lane 4: Eluate Lentil Chromatography
 Lane 5: Flow through during concentration lentil eluate
 Lane 6: Pool of E1 after Size Exclusion Chromatography

Fig.29

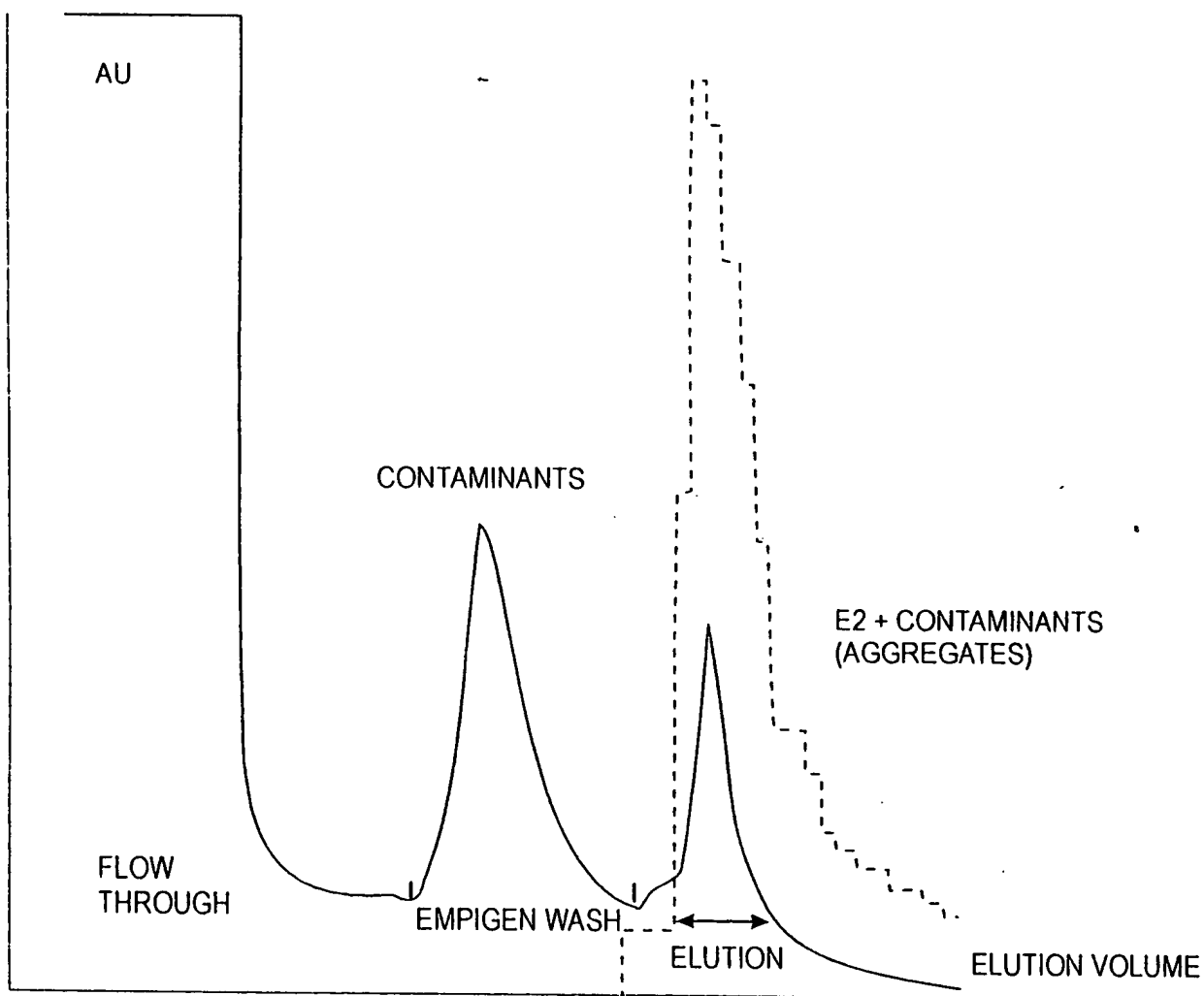
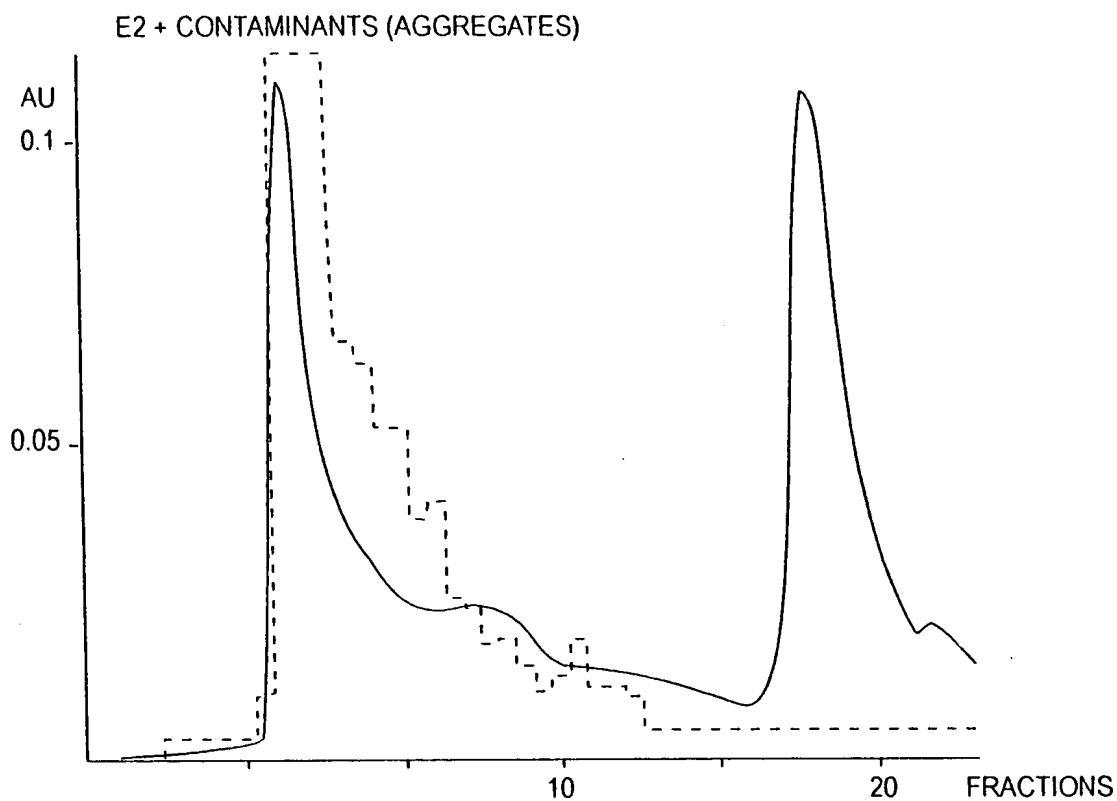


Fig. 30

NON - REDUCED

Fig. 31A



REDUCED

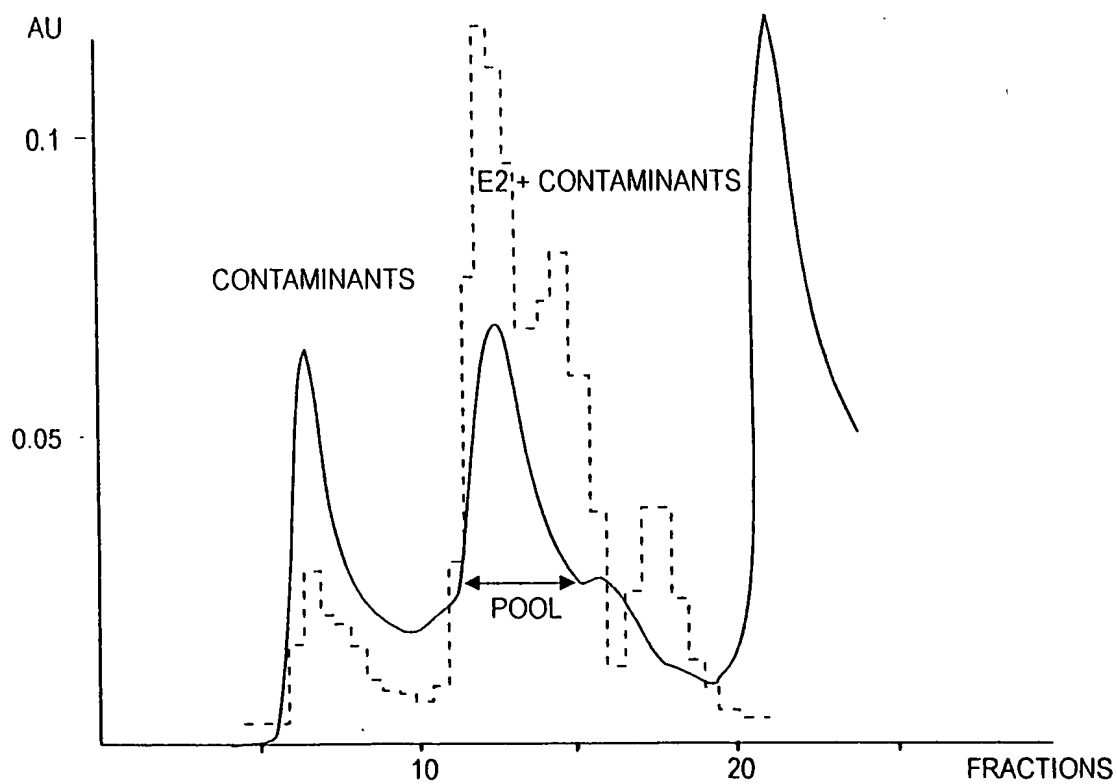


Fig. 31B

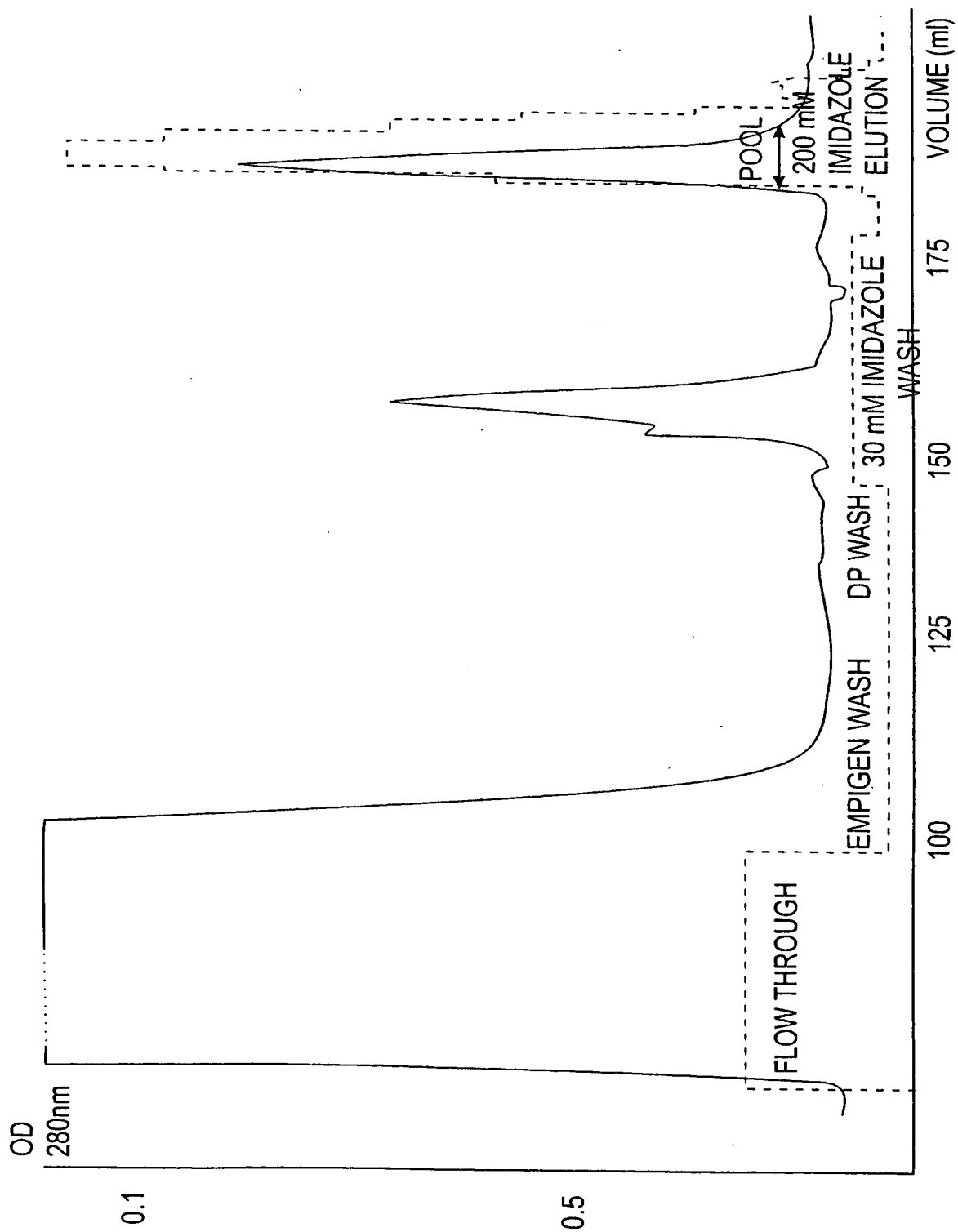
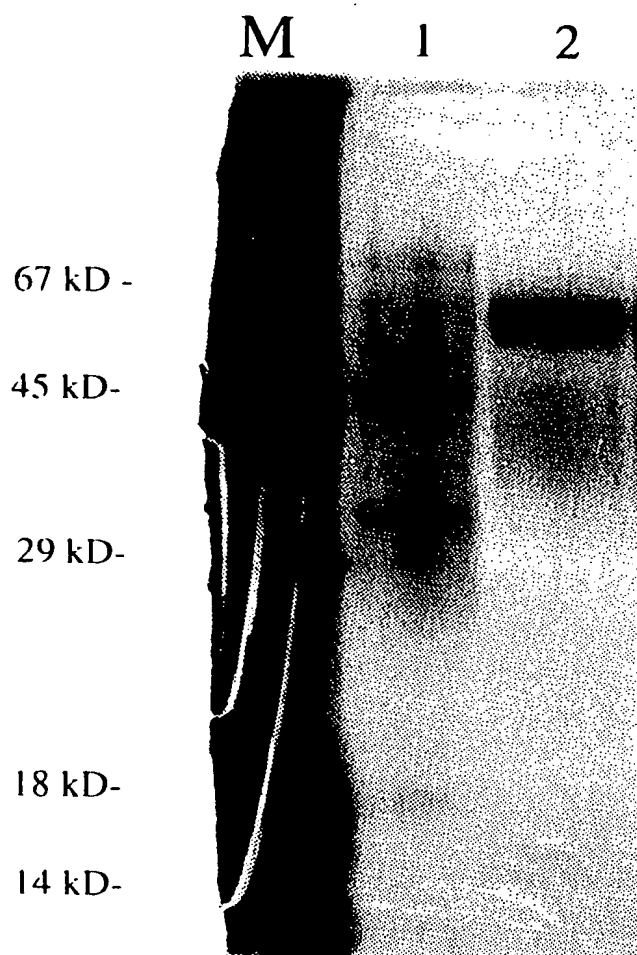


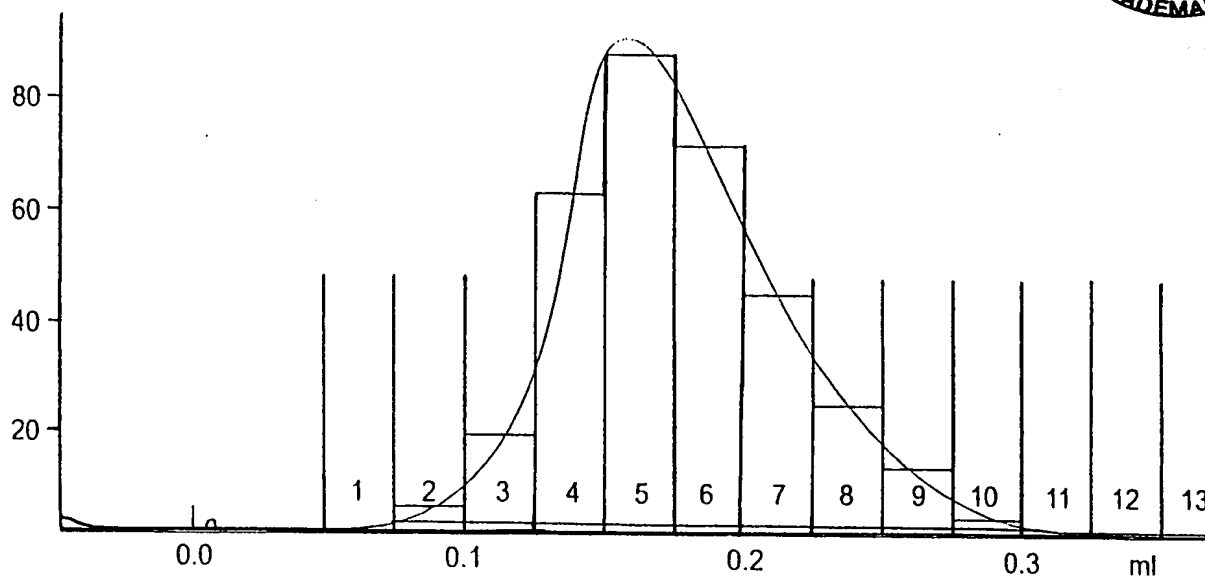
Fig. 32

SILVER STAIN OF PURIFIED E2



1. 30 mM IMIDAZOLE WASH Ni-IMAC
2. 0.5 ug E2

Fig.33



No.	Ret. (ml)	Peak start (ml)	Peak end (ml)	Dur (ml)	Area (ml*mAU)	Height (mAU)
1	-0.45	-0.46	-0.43	0.04	0.0976	4.579
2	1.55	0.75	3.26	2.51	796.4167	889.377
3	3.27	3.26	3.31	0.05	0.0067	0.224
4	3.33	3.32	3.33	0.02	0.0002	0.018

Total number of detected peaks = 4
 Total Area above baseline = 0.796522 ml*AU
 Total area in evaluated peaks = 0.796521 ml*AU
 Ratio peak area / total area = 0.999999
 Total peak duration = 2.613583 ml

Fig. 34

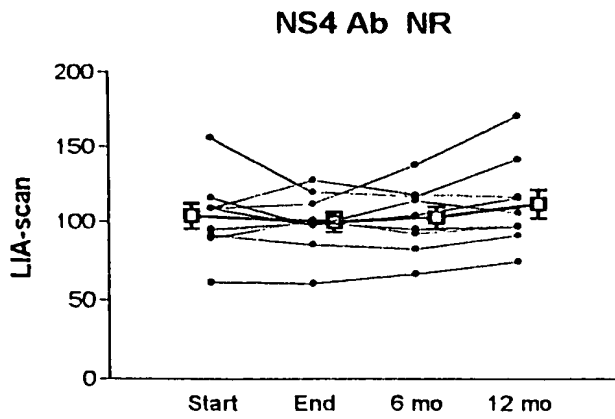


Fig. 35A-1

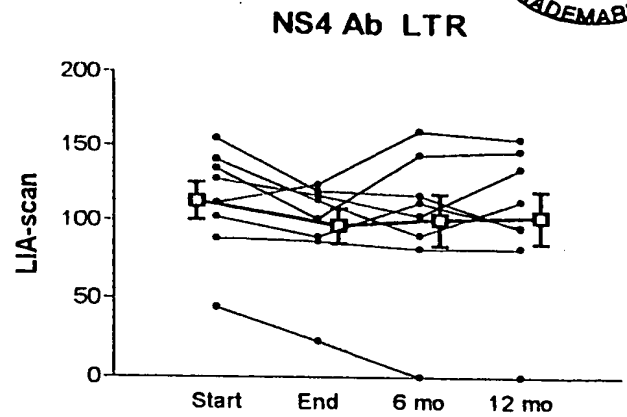


Fig. 35A-2

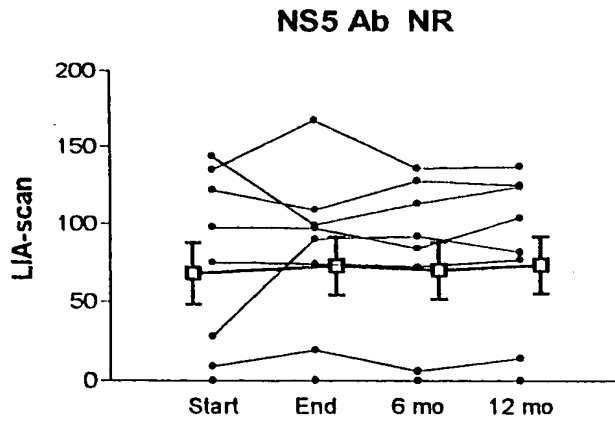


Fig. 35A-3

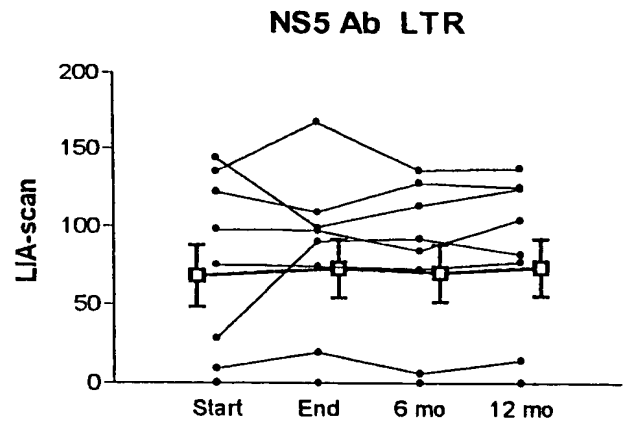


Fig. 35A-4

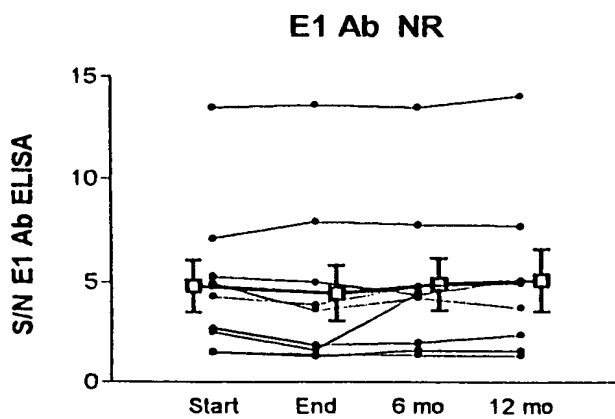


Fig. 35A-5

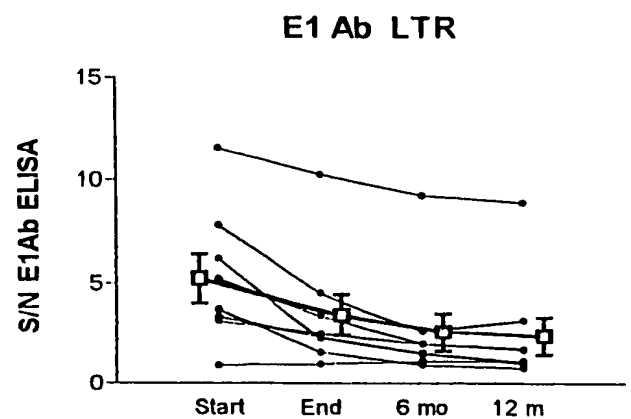


Fig. 35A-6

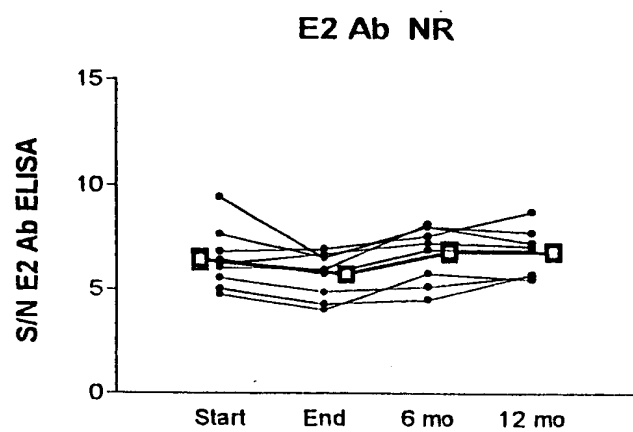


Fig. 35A-7

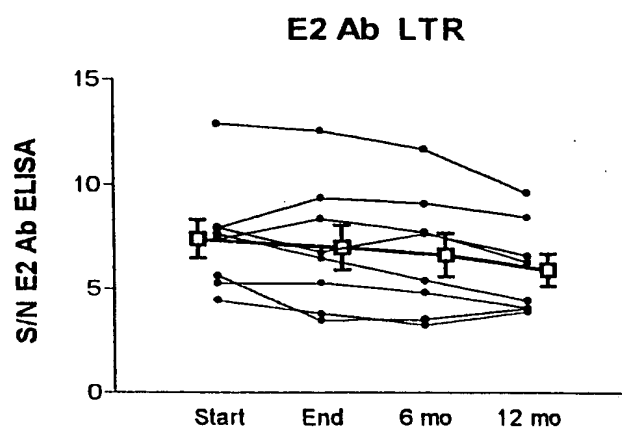


Fig. 35A-8

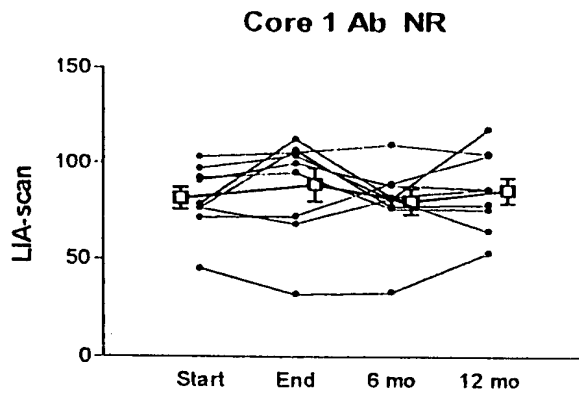


Fig. 35B-1

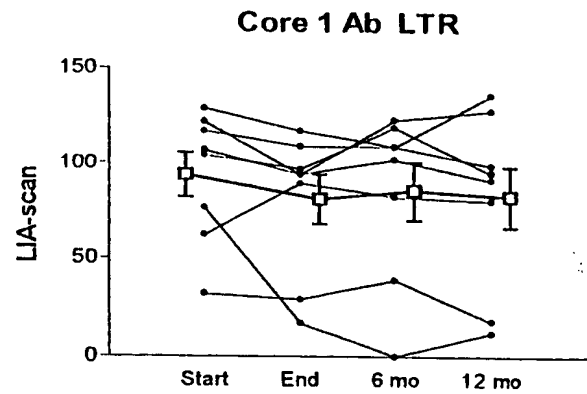


Fig. 35B-2

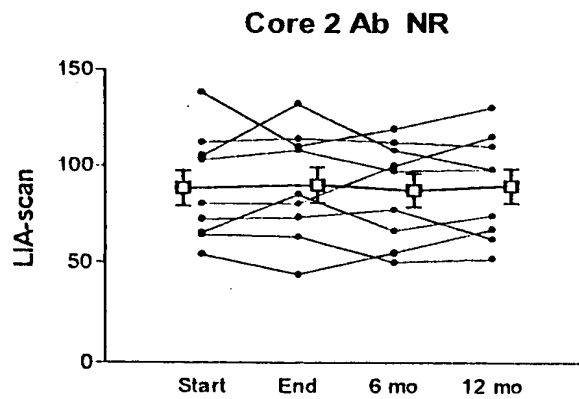


Fig. 35B-3

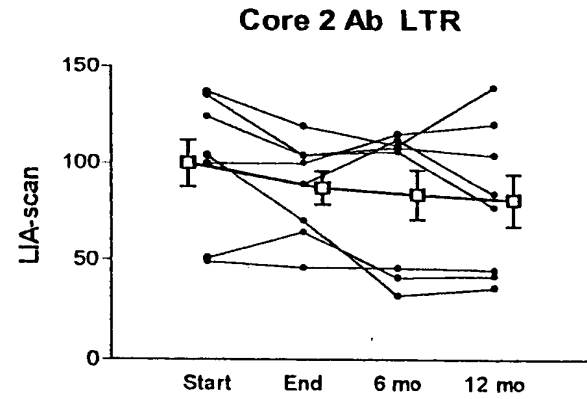


Fig. 35B-4

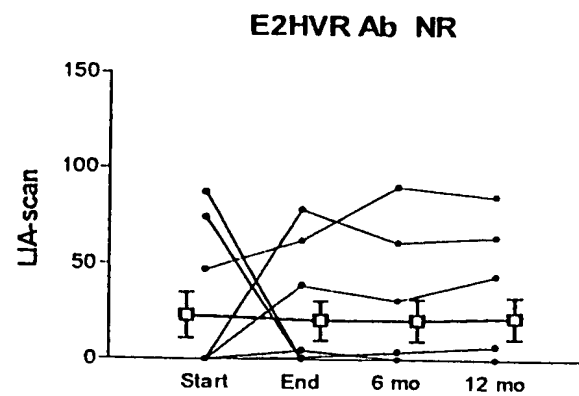


Fig. 35B-5

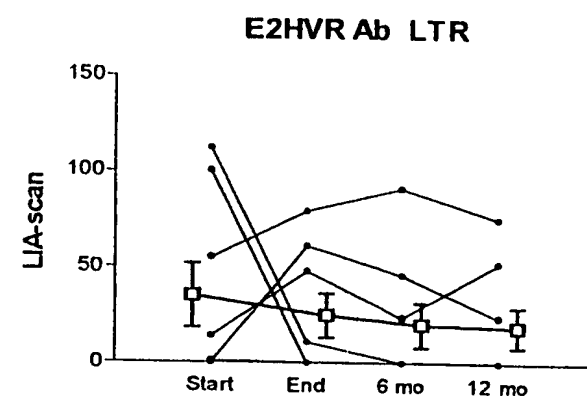


Fig. 35B-6

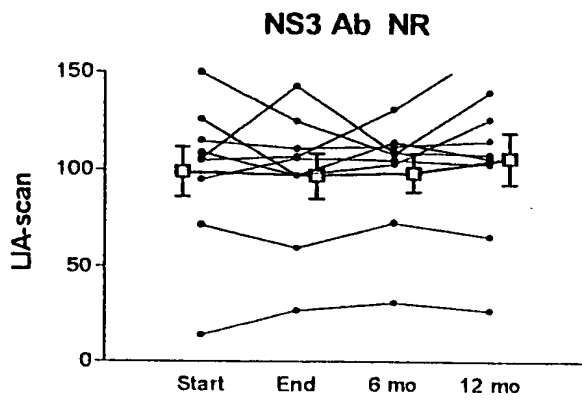


Fig. 35B-7

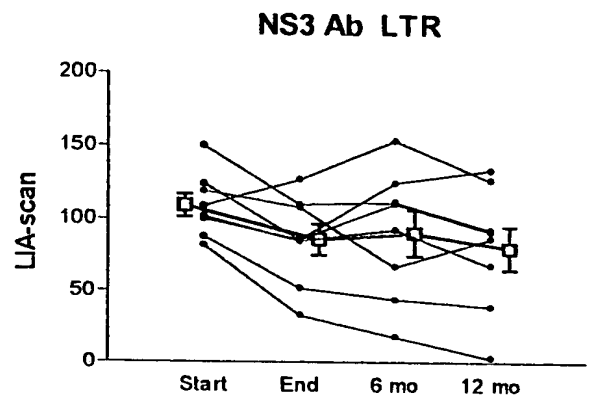


Fig. 35B-8

Fig. 36A

E1 Ab

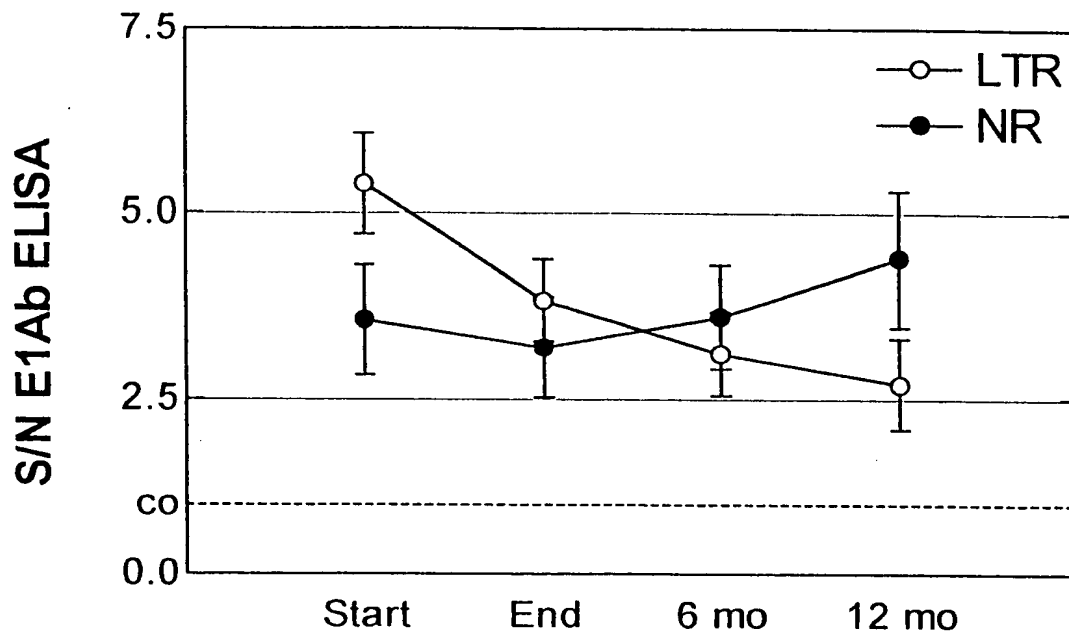


Fig. 36B

E2 Ab

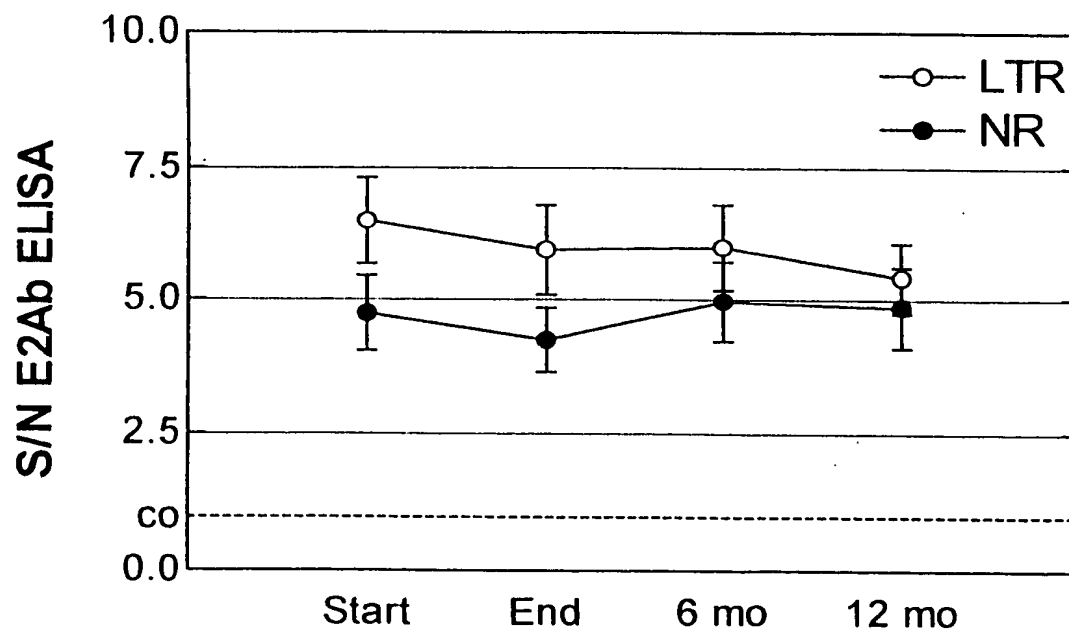


Fig. 37A

Non Responders

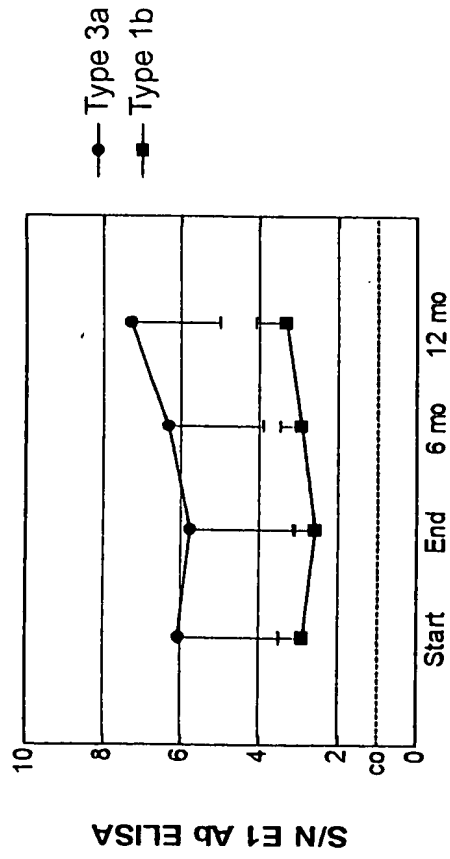


Fig. 37C

Type 1b

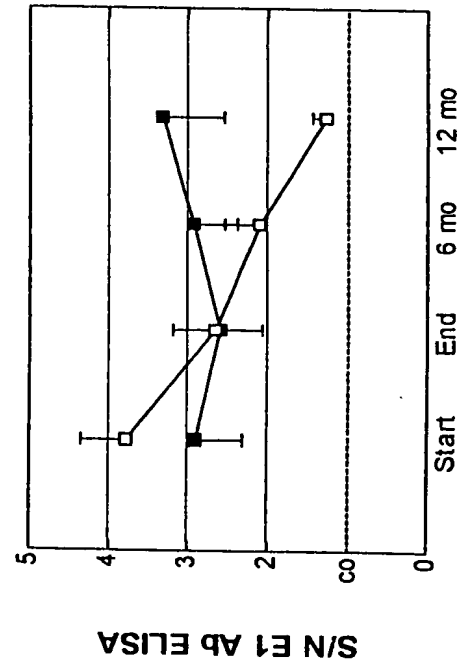


Fig. 37B

Long Term Responders

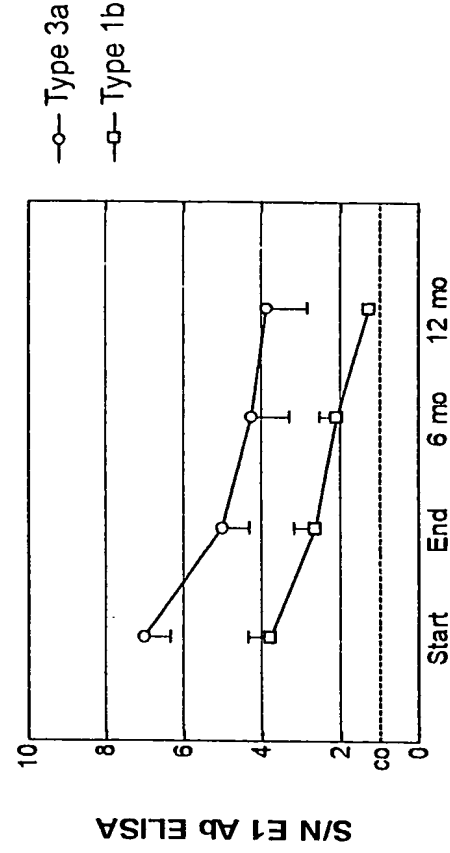


Fig. 37D

Type 3a

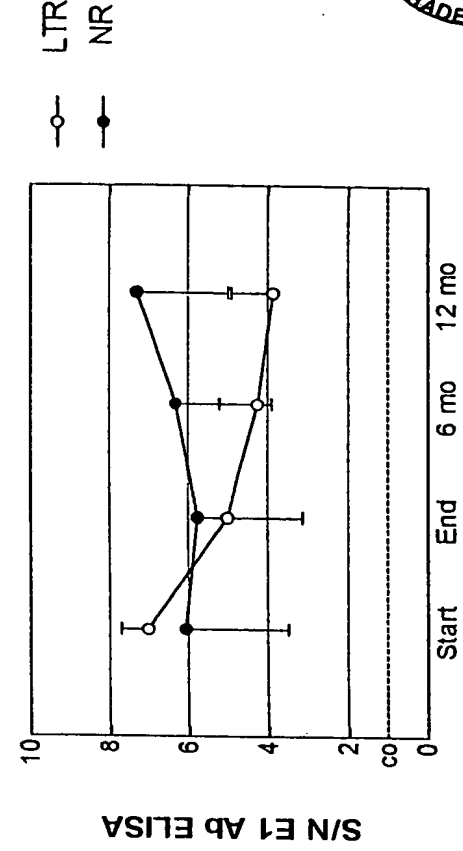
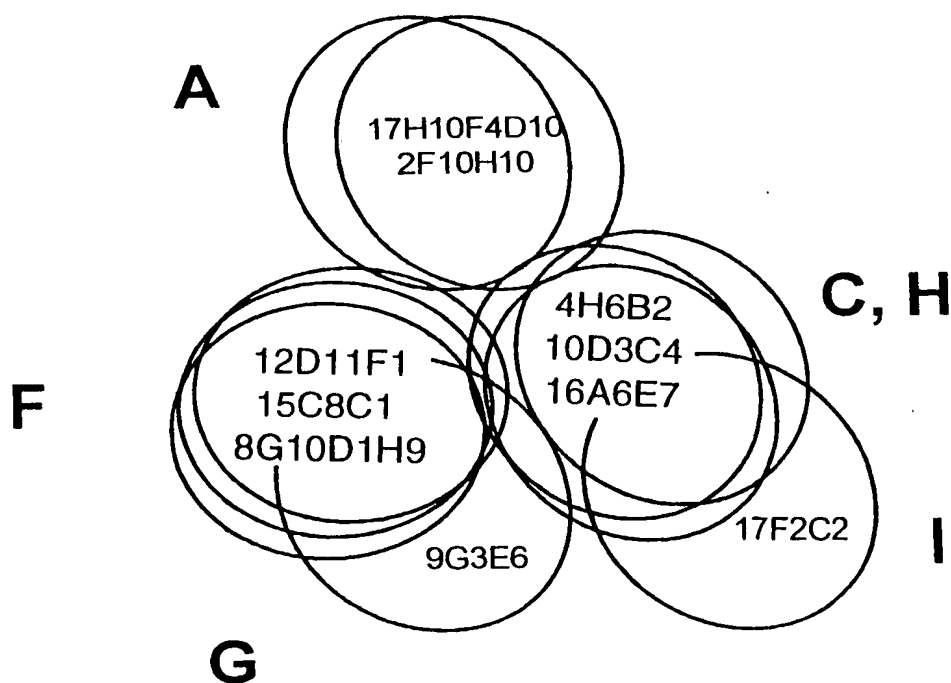


Fig. 38

Relative Map Positions of
anti-E2 monoclonal antibodies



PARTIAL TREATMENT OF HCV E2\E2s ENVELOPE PROTEINS BY PNGase F

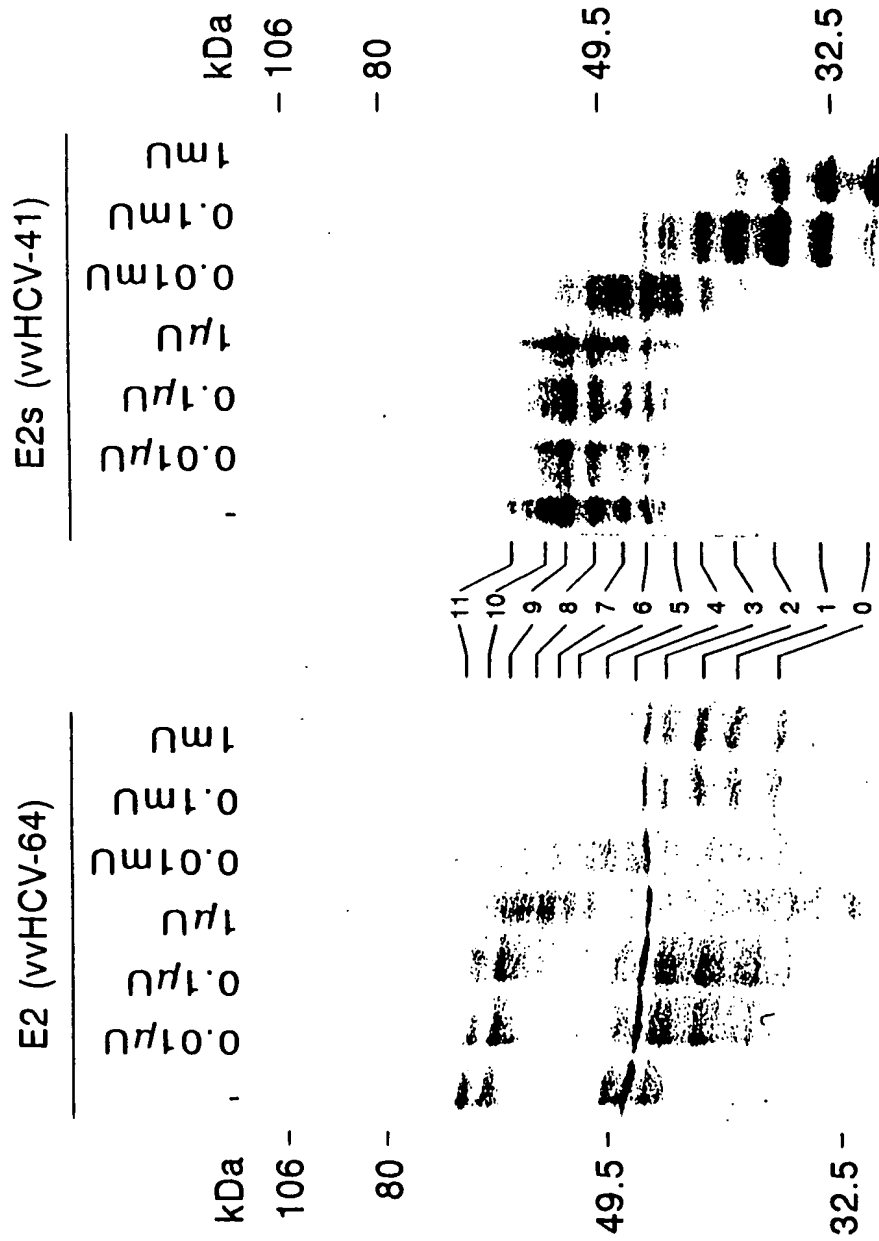


Fig.40

Fig. 41 *In Vitro* Mutagenesis of HCV E1 glycoprotein

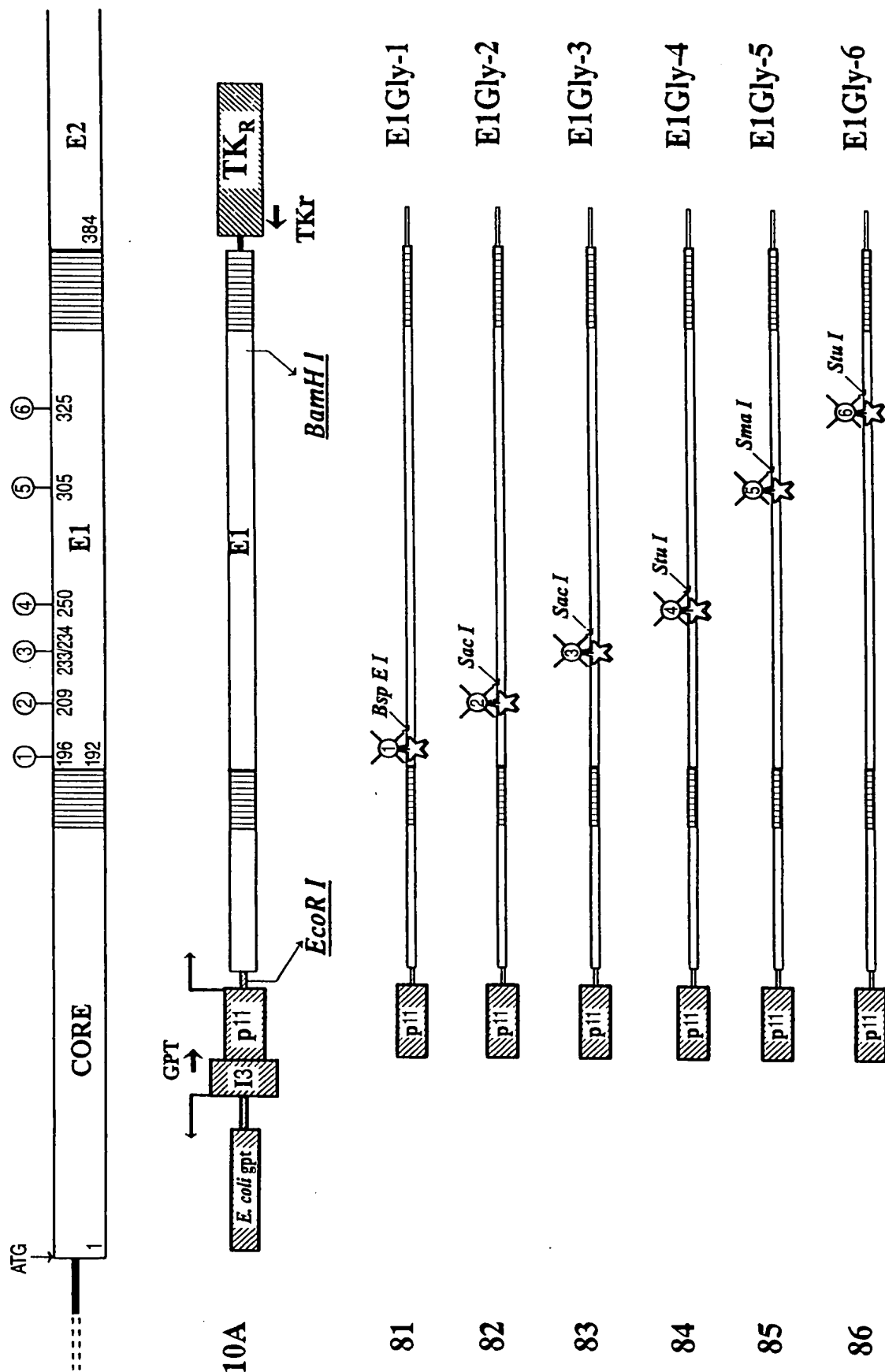
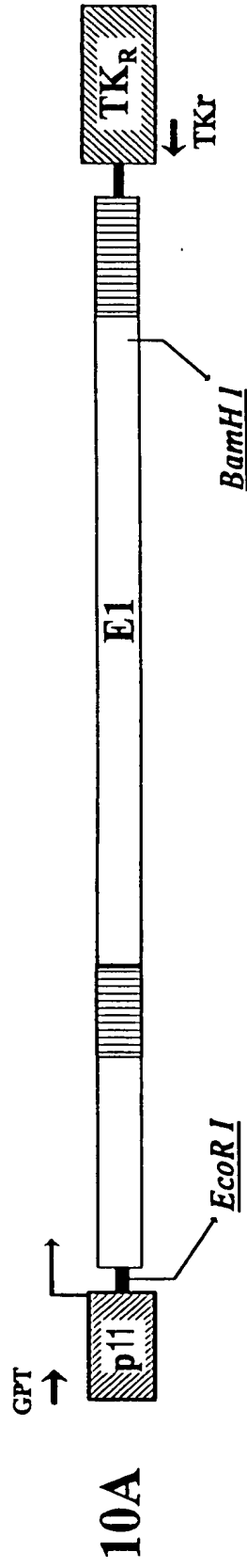
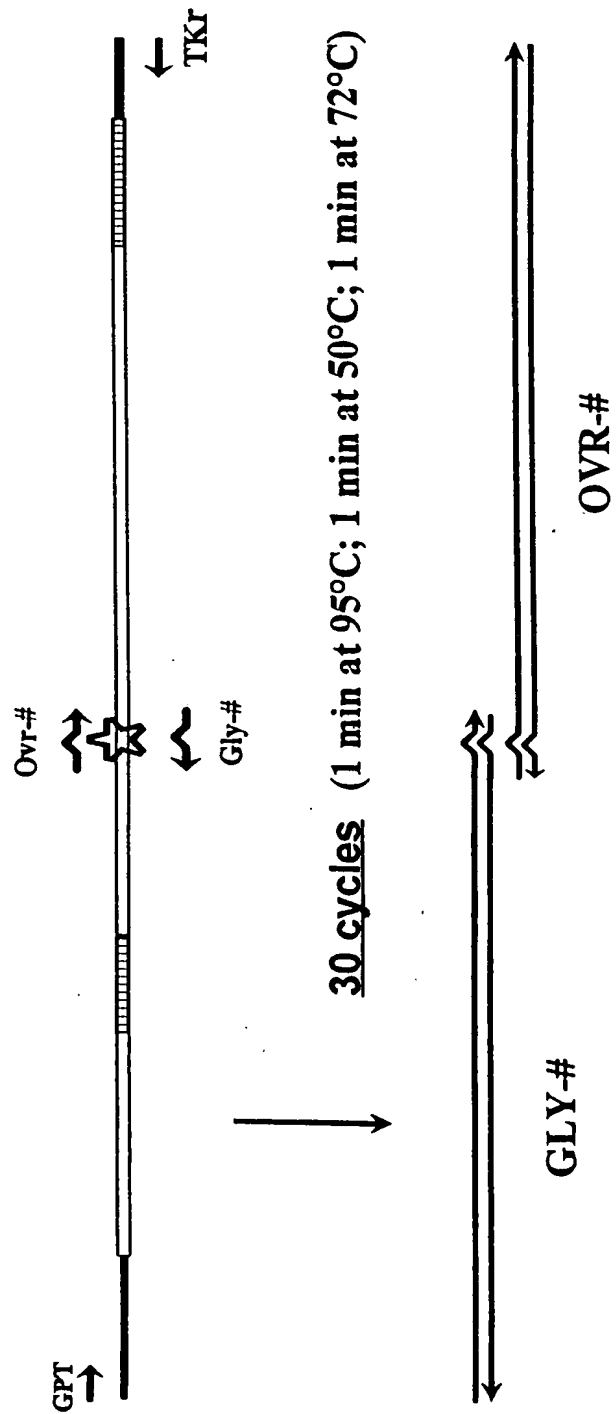


Fig. 42A *In Vitro* Mutagenesis of HCV E1 glycoprotein



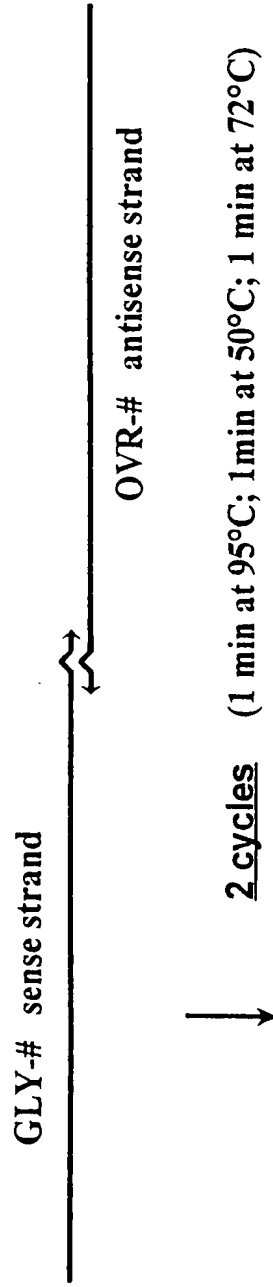
1. First step of PCR amplification (Gly-# and Ovr-# primers)



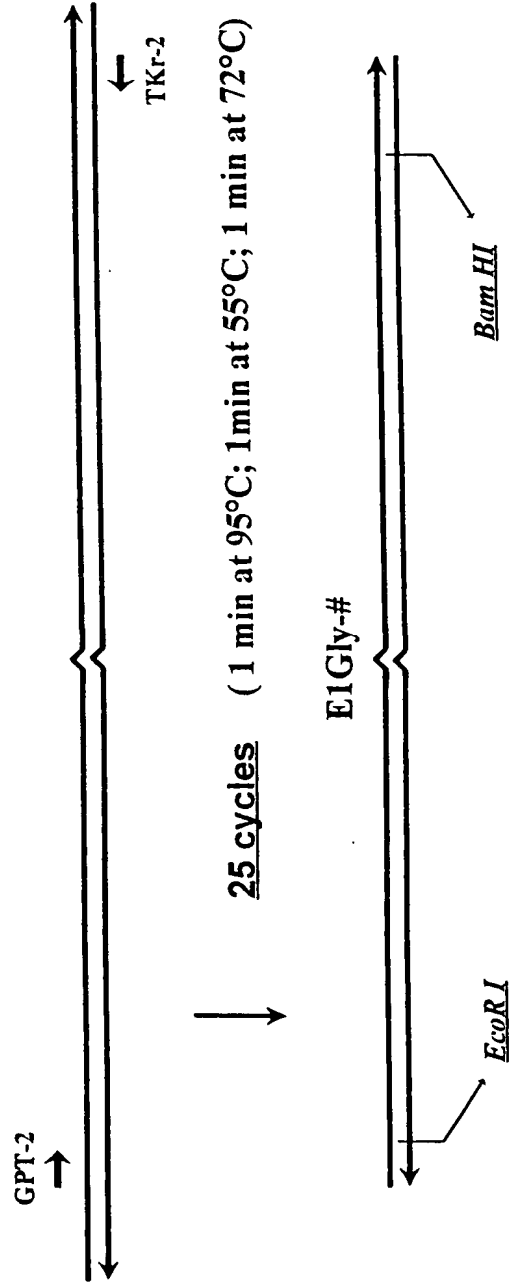
2. Overlap extension and nested PCR

Fig. 42B

a. Overlap extension



b. Nested PCR amplification (GPT-2 and TKr-2 primers)



The diagram illustrates the structure of the E1 gene and its various fragments. The full gene (10A) is shown at the top, with regions labeled CORE, E1, and TKR. The E1 region is further divided into segments 1 through 6. Below the full gene, fragments 81 through 86 are shown, each containing specific regions (OVR, GLY) and restriction enzyme sites (EcoRI, BamHI, TKr). The lengths of these fragments are indicated in nucleotides (nt).

Fragment	Regions	Length (nt)	Restriction Sites
10A	CORE, E1, TKR	384	EcoRI, BamHI, TKr
81	OVR-1, GLY-1	770	EcoRI, BamHI, TKr
82	OVR-2, GLY-2	630	EcoRI, BamHI, TKr
83	OVR-3, GLY-3	550	EcoRI, BamHI, TKr
84	OVR-4, GLY-4	500	EcoRI, BamHI, TKr
85	OVR-5, GLY-5	340	EcoRI, BamHI, TKr
86	OVR-6, GLY-6	280	EcoRI, BamHI, TKr

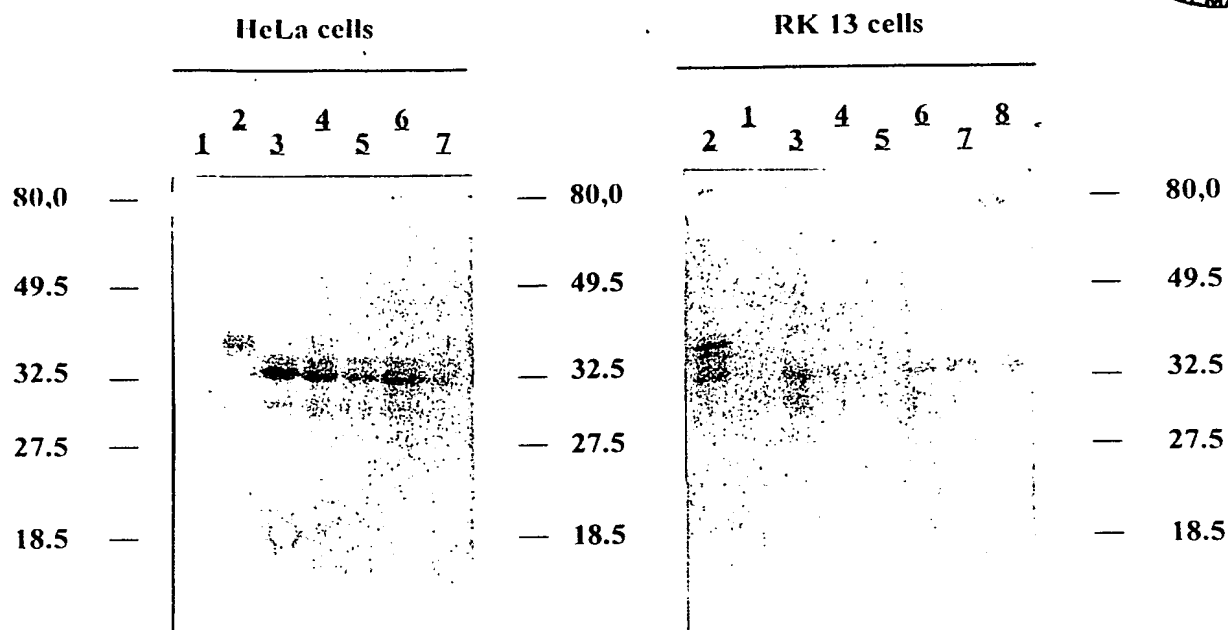


Fig. 44A

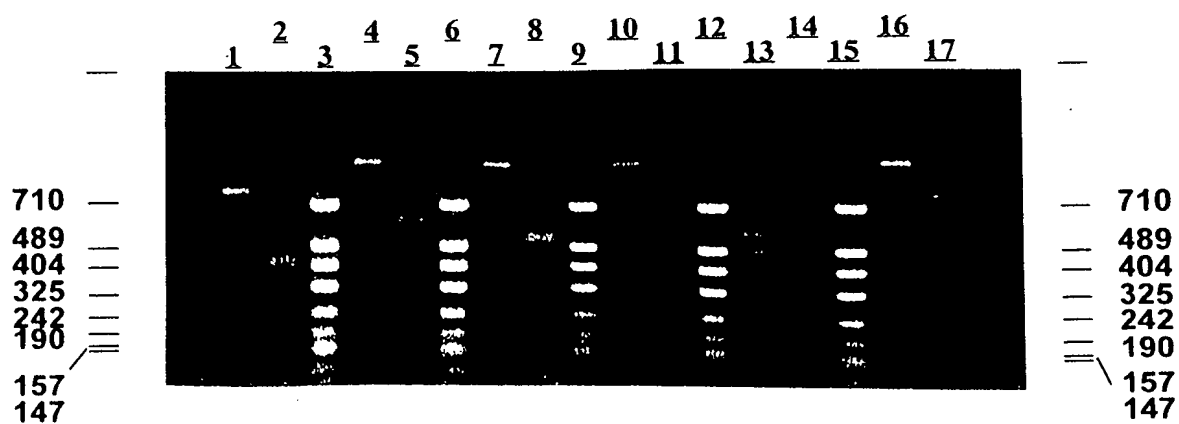


Fig. 44B

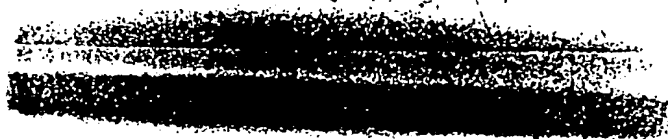


Fig.45

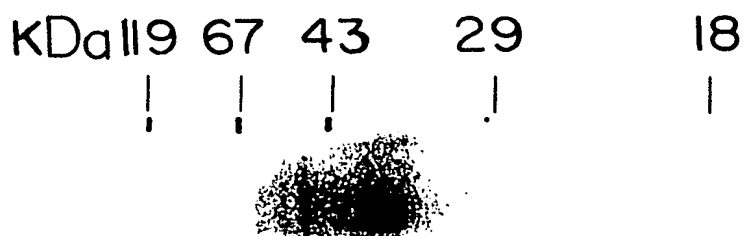


Fig.46